## STIC-Biotech/ChemLib

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Hutzell, Paula

Sent:

Monday, March 29, 2004 8:30 AM

To:

Holleran, Anne; STIC-Biotech/ChemLib

Cc:

Chan, Christina

Subject:

RE: RUSH sequence search for 09/477,082

## approved

----Original Message---

· From:

Holleran, Anne

Sent:

Friday, March 26, 2004 12:02 PM

To:

Hutzell, Paula

Cc:

Chan, Christina

Subject:

FW: RUSH sequence search for 09/477,082

----Original Message----

From:

Holleran, Anne

Sent:

Friday, March 26, 2004 12:01 PM

To:

Chan, Christina

Subject:

RUSH sequence search for 09/477,082

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following for 09/477,082

interference databases only search of SEQ ID NO: 1(na) interference databases only search of SEQ ID NO: 2(na)

commercial and interference database search of SEQ ID NO: 29, 30, 31, 32, 33, 34(na), these are primer sequences Please perform a Score/Length sequence search for the primer sequences (SEQ ID NO: 29-34) with a minimum hit length of 15 and a maximum hit length of 40, and a score over length value of 90% or greater

SEQ ID NO: 1 and SEQ ID NO: 2 are two different regions of the same gene

Anne Holleran

AU: 1642

Tel: (571) 272-0833 RM: Remsen, 3A14

mailbox: Remsen, 3C18

Searcher: Phone: Location: Date Picked Up: Date Completed: 3/3 Searcher Prep/Review: Clerical: Online time:

TYPE OF SEARCH: NA Sequences: AA Sequences:\_ Structures: Bibliographic:\_ Litigation:\_ Full text: Patent Family:

Other:\_

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):

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c5314	13.4	2	15		AX802132	0.893333
5315	13.4	2	15	6	BD208917	0.893333
8164	13	1.9	15	6	AX009449	0.866667
c1846	14.4	2.1	17	6	AX758412	0.847059
1847	14.4	2.1	17	8	ATH52680	9 0.847059
1848	14.4	2.1	17	8	ATH52681	0 0.847059
5316	13.4	2	16	6	AR080878	0.8375
c5317	13.4	2	16		BD266396	0.8375
c5318	13.4	2	16		BD104574	0.8375
1082	15	2.2	18		AX378655	0.833333
15795	12.4	1.9	15		A52100	0.826667
15796	12.4	1.9	15	L	A52101	0.826667
15797	12.4	1.9	15		A52128	0.826667
15798	12.4	1.9	15		A52129	0.826667
15799	12.4	1.9	15		A65237	0.826667
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15800			15			0.826667
15801	12.4	1.9			A66711	ļ
15802	12.4	1.9	15		A68206	0.826667
15803	12.4	1.9	15	6	A68260	0.826667

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7279	13.4	2	15	3 AAZ64339 0.893	
c7280	13.4	2	15	4 AAH74112 0.893	33
7281	13.4	2	15	6 AAD39760 0.893	33
7282	13.4	2	15	6 ABX01392 0.893	33
11340	13	1.9	15	3 AAZ48115 0.866	66
c2401	14.4	2.1	17	6 ABN07749 0.847	05
c2402	14.4	2.1	17	6 ABN07750 0.847	05
c2403	14.4	2.1	17	9 ADB41410 0.847	05
c17300	12.6	1.9	15	6 ABA03942 0	0.8
c7283	13.4	2	16	6 ABL31189 0.8	37
1374	15	2.2	18	6 ABK41196 0.833	33
21562	12.4	1.9	15	2 AAQ29530 0.826	66
21563	12.4	1.9	15	2 AAQ81114 0.826	66
21564	12.4	1.9	15	2 AAT55623 0.826	66
21565	12.4	1.9	15	2 AAT31819 0.826	66
c21566	12.4	1.9	15	2 AAX64708 0.826	66
21567	12.4	1.9	15	2 AAT37116 0.826	66
c21568	12.4	1.9	15	2 AAT50251 0.826	66
21569	12.4	1.9	15	2 AAV07762 0.826	66
21570	12.4	1.9	15	2 AAV07759 0.826	66
21571	12.4	1.9	15	2 AAV06230 0.826	66
21572	12.4	1.9	15	2 AAX33998 0.826	66
21573	12.4	1.9	15	2 AAV06801 0.826	
21574	12.4	1.9	15	2 AAV48551 0.826	66
21575	12.4	1.9	15	2 AAV06817 0.826	
21576	12.4	1.9	15	3 AAZ64338 0.826	
21577	12.4	1.9	15	3 AAA07813 0.826	
21578	12.4	1.9	15	4 AAH20310 0.826	
21579	12.4	1.9	15	4 AAF31459 0.826	
21580	12.4	1.9	15	4 AAF59902 0.826	
21581	12.4	1.9	15	4 AAF59905 0.826	
21582	12.4	1.9	15	4 AAF31566 0.826	
21583	12.4	1.9	15	4 AAF52237 0.826	
c21584	12.4	1.9	15	4 AAF52606 0.826	
21585	12.4	1.9	15	4 AAF52236 0.826	
c21586	12.4	1.9	15	4 AAF52607 0.826	
21587	12.4	1.9	15	4 AAH28548 0.826	
21588	12.4	1.9	15	4 AAF97971 0.826	
c21589	12.4	1.9	15	6 AAD41857 0.826	
21590	12.4	1.9	15	6 ABX01391 0.826	
21591	12.4	1.9	15	6 ABK98173 0.826	
21592	12.4	1.9	15	6 ABK98172 0.826	_
21593	12.4	1.9	15	6 ABK98144 0.826	
21594	12.4	1.9	15	7 ABX16342 0.826	
21595	12.4	1.9	15	9 ADC66181 0.826	
21596	12.4	1.9	15	9 ADC66180 0.826	_
c3721	14	2.1	17	7 ABT40012 0.823	
c3722	14	2.1	17	9 ADE25256 0.823	_
1660	14.8	2.2	18	2 AAX03843 0.822	

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c1093	14.4		<u> </u>		US-09-866-108A-7742	0.84705
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c9066	12.4	1.9	15	1	US-07-799-824-4	0.826667
c9067	12.4	1.9	15		US-07-976-103A-4	0.826667
c9068	12.4	1.9	15		US-08-363-240A-665	0.826667
9069	12.4	1.9	15		US-08-426-807-1	0.826667
9070	12.4	1.9	15		US-08-311-486C-16	0.826667
c9071	12.4	1.9	15		US-07-892-902-6	0.826667
9072	12.4	1.9	15		US-07-892-902-7	0.826667
c9073	12.4	1.9	15		US-08-473-481-4	0.826667
c9074	12.4	1.9	15		US-08-585-684B-202	0.826667
9075	12.4	1.9	15	2	US-08-459-434-1	0.826667
c9076	12.4	1.9	15	3	US-09-038-073-202	0.826667
c9077	12.4	1.9	15	3	US-08-338-352-5	0.826667
9078	12.4	1.9	15	4	US-09-202-294-1	0.826667
c9079	12.4	1.9	15	4	US-08-599-738A-4	0.826667
9080	12.4	1.9	15	4	US-09-612-531-4	0.826667
9081	12.4	1.9	15		US-09-612-531-8	0.826667
9082	12.4	1.9	. 15	4	US-09-612-531-9	0.826667
9083	12.4	1.9	15	4	US-09-612-531-10	0.826667
9084	12.4	1.9	15	4	US-09-612-531-14	0.826667
9085	12.4	1.9	15	4	US-09-612-531-15	0.826667
9086	12.4	1.9	15	4	US-09-612-531-16	0.826667
9087	12.4	1.9	15	4	US-09-612-531-17	0.826667
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9091	12.4	1.9	15	4	US-09-612-531-21	0.826667
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9094	12.4	1.9	15	4	US-09-612-531-24	0.826667
9095	12.4	1.9	15	4	US-09-612-531-25	0.826667
9096	12.4	1.9	15	4	US-09-142-212A-3	0.826667
9097	12.4	1.9	15	4	US-09-142-212A-4	0.826667
9098	12.4	1.9	15	4	US-09-142-212A-5	0.826667
9099	12.4	1.9	. 15	4	US-09-142-212A-6	0.826667
9100	12.4	1.9	15	4	US-09-142-212A-9	0.826667
9101	12.4	1.9	15	4	US-09-142-212A-13	0.826667
9102	12.4	1.9	15	4	US-09-349-040A-6	0.826667
9103	12.4	1.9	15	4	US-09-349-040A-7	0.826667
9104	12.4	1.9	15	4	US-09-349-040A-8	0.826667
9105	12.4	1.9	15	4	US-09-753-943D-3	0.826667
9106	12.4	1.9	15	4	US-09-753-943D-4	0.826667
9107	12.4	1.9	15	4	US-09-753-943D-6	0.826667
9108	12.4	1.9	15	. 4	US-09-753-943D-7	0.826667
9109	12.4	1.9	15	4	US-09-753-943D-8	0.826667
9110	12.4	1.9	15	4	US-09-753-943D-9	0.826667
c9111	12.4	1.9	15	4	US-09-753-943D-10	0.826667
c9112	12.4	1.9	15	4	US-09-753-943D-11	0.826667
c9113	12.4	1.9	15		US-09-753-943D-12	0.826667
c9114	12.4	1.9	. 15	4	US-09-753-943D-13	0.826667

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4093         13.4         2         15         9         US-09-274-553D-1174         0.89           c1318         14.4         2.1         17         9         US-09-866-108-7741         0.84           c1319         14.4         2.1         17         9         US-09-866-108-7742         0.84           c1320         14.4         2.1         17         10         US-09-730-289B-27         0.84           c1321         14.4         2.1         17         14         US-10-230-006-50         0.84           c1322         14.4         2.1         17         14         US-10-230-006-547         0.84           c4094         13.4         2.1         17         15         US-10-230-006-547         0.84           c4094         13.4         2         16         15         US-10-297-068-678         0.34           c4094         13.4         2         16         15         US-10-297-068-678         0.34           12708         12.4         1.9         15         9         US-09-504-231A-1173         0.82           12709         12.4         1.9         15         14         US-10-247-893-4         0.82           12710         12.4 </th <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>							
Result   No.   Score   Match   Length   DB   ID   S/L				IES			
No.   Score   Match   Length   DB   ID   S/L			%				
4092 13.4 2 15 9 US-09-504-231A-1174 0.89: 4093 13.4 2 15 9 US-09-866-108-7741 0.84: c1318 14.4 2.1 17 9 US-09-866-108-7741 0.84: c1319 14.4 2.1 17 9 US-09-866-108-7742 0.84: c1320 14.4 2.1 17 10 US-09-730-289B-27 0.84: c1321 14.4 2.1 17 14 US-10-230-006-50 0.84: c1322 14.4 2.1 17 14 US-10-230-006-50 0.84: c1323 14.4 2.1 17 15 US-10-300-683-252 0.84: c4094 13.4 2 16 15 US-10-300-683-252 0.84: c4094 13.4 2 16 15 US-10-300-686-78 0.34: c4094 13.4 2 16 15 US-10-300-686-78 0.34: c4094 13.4 2 16 15 US-10-300-683-252 0.84: c4094 13.4 2 19 15 9 US-09-274-553D-1173 0.82: c4094 13.4 2 19 15 9 US-09-274-553D-1173 0.82: c4094 13.4 1.9 15 14 US-10-247-893-4 0.82: c4094 13.4 1.9 15 14 US-10-247-893-9 0.82: c4094 13.4 1.9 15 14 US-10-247-893-9 0.82: c4094 13.4 1.9 15 14 US-10-247-893-16 0.82: c4094 13.4 1.9 15 14 US-10-247-893-19 0.82: c4094 13.4 1.9 15 14 US-10-247-893-20 0.82: c4094 13.4 1.9 15 14 US-10-247-893-21 0.82: c4094 13.4 1.9 15 14 US-10-247-893-21 0.82: c4094 13.4 1.9 15 14 US-10-247-893-21 0.82: c4094 13.4 1.9 15 14 US-10-247-893-20 0.82: c4094 13.4 1.9 15 14 US-10-247-8	Result		Query				
4093         13.4         2         15         9         US-09-274-553D-1174         0.89           c1318         14.4         2.1         17         9         US-09-866-108-7741         0.84'           c1319         14.4         2.1         17         9         US-09-866-108-7742         0.84'           c1320         14.4         2.1         17         10         US-09-730-289B-27         0.84'           c1321         14.4         2.1         17         14         US-10-230-006-50         0.84'           c1322         14.4         2.1         17         14         US-10-230-006-547         0.84'           c4094         13.4         2.1         17         15         US-10-230-006-547         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.82'           12708         12.4         1.9         15         9         US-09-504-231A-1173         0.82'           12709	No.	Score	Match	Length	DB	ID	S/L
4093         13.4         2         15         9         US-09-274-553D-1174         0.89           c1318         14.4         2.1         17         9         US-09-866-108-7741         0.84'           c1319         14.4         2.1         17         9         US-09-866-108-7742         0.84'           c1320         14.4         2.1         17         10         US-09-730-289B-27         0.84'           c1321         14.4         2.1         17         14         US-10-230-006-50         0.84'           c1322         14.4         2.1         17         14         US-10-230-006-547         0.84'           c4094         13.4         2.1         17         15         US-10-230-006-547         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.84'           c4094         13.4         2         16         15         US-10-297-068-678         0.82'           12708         12.4         1.9         15         9         US-09-504-231A-1173         0.82'           12709							
c1318         14.4         2.1         17         9         US-09-866-108-7741         0.84           c1319         14.4         2.1         17         9         US-09-866-108-7742         0.84*           c1320         14.4         2.1         17         10         US-09-730-289B-27         0.84*           c1321         14.4         2.1         17         14         US-10-230-006-50         0.84*           c1322         14.4         2.1         17         14         US-10-230-006-50         0.84*           c4094         13.4         2.1         17         15         US-10-300-683-252         0.84*           c4094         13.4         2.1         17         15         US-10-300-683-252         0.84*           c4094         13.4         2.1         17         15         US-10-297-068-678         0.82*           690         15         2.2         18         12         US-10-333-429-444         0.83*           12708         12.4         1.9         15         9         US-09-274-553D-1173         0.82*           12710         12.4         1.9         15         14         US-10-247-893-4         0.82*           12711	4092	13.4			9	US-09-504-231A-1174	0.893333
c1319         14.4         2.1         17         9         US-09-866-108-7742         0.84*           c1320         14.4         2.1         17         10         US-09-730-289B-27         0.84*           c1321         14.4         2.1         17         14         US-10-230-006-50         0.84*           c1322         14.4         2.1         17         14         US-10-230-006-547         0.84*           c1323         14.4         2.1         17         15         US-10-300-683-252         0.84*           c4094         13.4         2         16         15         US-10-297-068-678         0.84*           690         15         2.2         18         12         US-10-297-068-678         0.82*           12708         12.4         1.9         15         9         US-09-504-231A-1173         0.82*           12709         12.4         1.9         15         9         US-09-274-553D-1173         0.82*           12710         12.4         1.9         15         14         US-10-247-893-4         0.82*           12711         12.4         1.9         15         14         US-10-247-893-8         0.82*           12712	4093	13.4	2	15	9	US-09-274-553D-1174	0.893333
1320         14.4         2.1         17         10 US-09-730-289B-27         0.84           c1321         14.4         2.1         17         14 US-10-230-006-50         0.84*           c1322         14.4         2.1         17         14 US-10-230-006-547         0.84*           1323         14.4         2.1         17         15 US-10-300-683-252         0.84*           c4094         13.4         2         16         15 US-10-300-683-252         0.84*           690         15         2.2         18         12 US-10-333-429-444         0.83*           12708         12.4         1.9         15         9 US-09-504-231A-1173         0.82*           12709         12.4         1.9         15         9 US-09-274-553D-1173         0.82*           12710         12.4         1.9         15         14 US-10-247-893-4         0.82*           12711         12.4         1.9         15         14 US-10-247-893-8         0.82*           12711         12.4         1.9         15         14 US-10-247-893-9         0.82*           12712         12.4         1.9         15         14 US-10-247-893-10         0.82*           12713         12.4         1		14.4	2.1	17		1	0.847059
c1321         14.4         2.1         17         14 US-10-230-006-50         0.84           c1322         14.4         2.1         17         14 US-10-230-006-547         0.84           1323         14.4         2.1         17         15 US-10-300-683-252         0.84           c4094         13.4         2         16         15 US-10-297-068-678         0.3           690         15         2.2         18         12 US-10-333-429-444         0.83           12708         12.4         1.9         15         9 US-09-504-231A-1173         0.82           12709         12.4         1.9         15         9 US-09-274-553D-1173         0.82           12710         12.4         1.9         15         14 US-10-247-893-4         0.82           12711         12.4         1.9         15         14 US-10-247-893-8         0.82           12712         12.4         1.9         15         14 US-10-247-893-8         0.82           12713         12.4         1.9         15         14 US-10-247-893-10         0.82           12713         12.4         1.9         15         14 US-10-247-893-10         0.82           12716         12.4         1.9	c1319	14.4	2.1	17	9	US-09-866-108-7742	0.847059
c1322         14.4         2.1         17         14 US-10-230-006-547         0.84           1323         14.4         2.1         17         15 US-10-300-683-252         0.84           c4094         13.4         2         16         15 US-10-297-068-678         0.3           690         15         2.2         18         12 US-10-333-429-444         0.83           12708         12.4         1.9         15         9 US-09-504-231A-1173         0.82           12709         12.4         1.9         15         9 US-09-274-553D-1173         0.82           12710         12.4         1.9         15         14 US-10-247-893-4         0.82           12711         12.4         1.9         15         14 US-10-247-893-4         0.82           12711         12.4         1.9         15         14 US-10-247-893-8         0.82           12712         12.4         1.9         15         14 US-10-247-893-10         0.82           12713         12.4         1.9         15         14 US-10-247-893-10         0.82           12714         12.4         1.9         15         14 US-10-247-893-10         0.82           12715         12.4         1.9	1320	14.4	2.1	17		l	0.847059
1323         14.4         2.1         17         15         US-10-300-683-252         0.84           c4094         13.4         2         16         15         US-10-297-068-678         0.3           690         15         2.2         18         12         US-10-333-429-444         0.83           12708         12.4         1.9         15         9         US-09-504-231A-1173         0.820           12709         12.4         1.9         15         9         US-09-274-553D-1173         0.820           12710         12.4         1.9         15         14         US-10-247-893-4         0.820           12711         12.4         1.9         15         14         US-10-247-893-8         0.820           12712         12.4         1.9         15         14         US-10-247-893-9         0.820           12713         12.4         1.9         15         14         US-10-247-893-10         0.820           12714         12.4         1.9         15         14         US-10-247-893-14         0.820           12715         12.4         1.9         15         14         US-10-247-893-15         0.820           12716         12.4<		14.4	2.1		14	US-10-230-006-50	0.847059
c4094         13.4         2         16         15 US-10-297-068-678         0.3           690         15         2.2         18         12 US-10-333-429-444         0.83           12708         12.4         1.9         15         9 US-09-504-231A-1173         0.820           12709         12.4         1.9         15         9 US-09-274-553D-1173         0.820           12710         12.4         1.9         15         14 US-10-247-893-4         0.820           12711         12.4         1.9         15         14 US-10-247-893-8         0.820           12712         12.4         1.9         15         14 US-10-247-893-8         0.820           12713         12.4         1.9         15         14 US-10-247-893-8         0.820           12713         12.4         1.9         15         14 US-10-247-893-10         0.820           12714         12.4         1.9         15         14 US-10-247-893-10         0.820           12715         12.4         1.9         15         14 US-10-247-893-15         0.820           12716         12.4         1.9         15         14 US-10-247-893-15         0.820           12717         12.4         1.9 </td <td></td> <td></td> <td></td> <td>17</td> <td>14</td> <td>US-10-230-006-547</td> <td>0.847059</td>				17	14	US-10-230-006-547	0.847059
690         15         2.2         18         12 US-10-333-429-444         0.83:           12708         12.4         1.9         15         9 US-09-504-231A-1173         0.820           12709         12.4         1.9         15         9 US-09-274-553D-1173         0.820           12710         12.4         1.9         15         14 US-10-247-893-4         0.820           12711         12.4         1.9         15         14 US-10-247-893-8         0.820           12712         12.4         1.9         15         14 US-10-247-893-9         0.820           12713         12.4         1.9         15         14 US-10-247-893-10         0.820           12714         12.4         1.9         15         14 US-10-247-893-10         0.820           12714         12.4         1.9         15         14 US-10-247-893-10         0.820           12715         12.4         1.9         15         14 US-10-247-893-10         0.820           12715         12.4         1.9         15         14 US-10-247-893-14         0.820           12716         12.4         1.9         15         14 US-10-247-893-16         0.820           12717         12.4					15	US-10-300-683-252	0.847059
12708         12.4         1.9         15         9         US-09-504-231A-1173         0.820           12709         12.4         1.9         15         9         US-09-274-553D-1173         0.820           12710         12.4         1.9         15         14         US-10-247-893-4         0.820           12711         12.4         1.9         15         14         US-10-247-893-8         0.820           12712         12.4         1.9         15         14         US-10-247-893-9         0.820           12713         12.4         1.9         15         14         US-10-247-893-10         0.820           12714         12.4         1.9         15         14         US-10-247-893-10         0.820           12715         12.4         1.9         15         14         US-10-247-893-10         0.820           12716         12.4         1.9         15         14         US-10-247-893-10         0.820           12717         12.4         1.9         15         14         US-10-247-893-15         0.820           12717         12.4         1.9         15         14         US-10-247-893-18         0.820           12719         <							0.8375
12709         12.4         1.9         15         9         US-09-274-553D-1173         0.820           12710         12.4         1.9         15         14         US-10-247-893-4         0.820           12711         12.4         1.9         15         14         US-10-247-893-8         0.820           12712         12.4         1.9         15         14         US-10-247-893-9         0.820           12713         12.4         1.9         15         14         US-10-247-893-10         0.820           12714         12.4         1.9         15         14         US-10-247-893-10         0.820           12715         12.4         1.9         15         14         US-10-247-893-10         0.820           12715         12.4         1.9         15         14         US-10-247-893-14         0.820           12716         12.4         1.9         15         14         US-10-247-893-15         0.820           12717         12.4         1.9         15         14         US-10-247-893-17         0.820           12718         12.4         1.9         15         14         US-10-247-893-18         0.820           12729 <td< td=""><td></td><td></td><td></td><td><del></del></td><td></td><td></td><td>0.833333</td></td<>				<del></del>			0.833333
12710         12.4         1.9         15         14         US-10-247-893-4         0.826           12711         12.4         1.9         15         14         US-10-247-893-8         0.826           12712         12.4         1.9         15         14         US-10-247-893-9         0.826           12713         12.4         1.9         15         14         US-10-247-893-10         0.826           12714         12.4         1.9         15         14         US-10-247-893-10         0.826           12715         12.4         1.9         15         14         US-10-247-893-14         0.826           12716         12.4         1.9         15         14         US-10-247-893-15         0.826           12717         12.4         1.9         15         14         US-10-247-893-16         0.826           12717         12.4         1.9         15         14         US-10-247-893-16         0.826           12718         12.4         1.9         15         14         US-10-247-893-17         0.826           12719         12.4         1.9         15         14         US-10-247-893-18         0.826           12720         1				1			0.826667
12711         12.4         1.9         15         14         US-10-247-893-8         0.826           12712         12.4         1.9         15         14         US-10-247-893-9         0.826           12713         12.4         1.9         15         14         US-10-247-893-10         0.826           12714         12.4         1.9         15         14         US-10-247-893-14         0.826           12715         12.4         1.9         15         14         US-10-247-893-15         0.826           12716         12.4         1.9         15         14         US-10-247-893-15         0.826           12717         12.4         1.9         15         14         US-10-247-893-16         0.826           12718         12.4         1.9         15         14         US-10-247-893-17         0.826           12719         12.4         1.9         15         14         US-10-247-893-19         0.826           12720         12.4         1.9         15         14         US-10-247-893-20         0.826           12721         12.4         1.9         15         14         US-10-247-893-21         0.826           12722							0.826667
12712         12.4         1.9         15         14         US-10-247-893-9         0.826           12713         12.4         1.9         15         14         US-10-247-893-10         0.826           12714         12.4         1.9         15         14         US-10-247-893-14         0.826           12715         12.4         1.9         15         14         US-10-247-893-15         0.826           12716         12.4         1.9         15         14         US-10-247-893-16         0.826           12717         12.4         1.9         15         14         US-10-247-893-16         0.826           12718         12.4         1.9         15         14         US-10-247-893-17         0.826           12719         12.4         1.9         15         14         US-10-247-893-17         0.826           12719         12.4         1.9         15         14         US-10-247-893-18         0.826           12720         12.4         1.9         15         14         US-10-247-893-19         0.826           12721         12.4         1.9         15         14         US-10-247-893-20         0.826           12722 <td< td=""><td></td><td></td><td></td><td>1</td><td></td><td></td><td>0.826667</td></td<>				1			0.826667
12713         12.4         1.9         15         14 US-10-247-893-10         0.826           12714         12.4         1.9         15         14 US-10-247-893-14         0.826           12715         12.4         1.9         15         14 US-10-247-893-15         0.826           12716         12.4         1.9         15         14 US-10-247-893-16         0.826           12717         12.4         1.9         15         14 US-10-247-893-17         0.826           12718         12.4         1.9         15         14 US-10-247-893-17         0.826           12719         12.4         1.9         15         14 US-10-247-893-17         0.826           12719         12.4         1.9         15         14 US-10-247-893-18         0.826           12720         12.4         1.9         15         14 US-10-247-893-19         0.826           12721         12.4         1.9         15         14 US-10-247-893-19         0.826           12721         12.4         1.9         15         14 US-10-247-893-20         0.826           12722         12.4         1.9         15         14 US-10-247-893-21         0.826           12723         12.4 <t< td=""><td></td><td></td><td></td><td></td><td></td><td>L</td><td>0.826667</td></t<>						L	0.826667
12714         12.4         1.9         15         14 US-10-247-893-14         0.820           12715         12.4         1.9         15         14 US-10-247-893-15         0.820           12716         12.4         1.9         15         14 US-10-247-893-16         0.820           12717         12.4         1.9         15         14 US-10-247-893-17         0.820           12718         12.4         1.9         15         14 US-10-247-893-18         0.820           12719         12.4         1.9         15         14 US-10-247-893-18         0.820           12720         12.4         1.9         15         14 US-10-247-893-19         0.820           12720         12.4         1.9         15         14 US-10-247-893-19         0.820           12721         12.4         1.9         15         14 US-10-247-893-19         0.820           12721         12.4         1.9         15         14 US-10-247-893-20         0.820           12722         12.4         1.9         15         14 US-10-247-893-21         0.820           12723         12.4         1.9         15         14 US-10-247-893-23         0.820           12724         12.4 <t< td=""><td>12712</td><td>12.4</td><td>1.9</td><td></td><td>14</td><td>US-10-247-893-9</td><td>0.826667</td></t<>	12712	12.4	1.9		14	US-10-247-893-9	0.826667
12715         12.4         1.9         15         14         US-10-247-893-15         0.826           12716         12.4         1.9         15         14         US-10-247-893-16         0.826           12717         12.4         1.9         15         14         US-10-247-893-17         0.826           12718         12.4         1.9         15         14         US-10-247-893-18         0.826           12719         12.4         1.9         15         14         US-10-247-893-19         0.826           12720         12.4         1.9         15         14         US-10-247-893-19         0.826           12721         12.4         1.9         15         14         US-10-247-893-20         0.826           12721         12.4         1.9         15         14         US-10-247-893-21         0.826           12722         12.4         1.9         15         14         US-10-247-893-22         0.826           12723         12.4         1.9         15         14         US-10-247-893-23         0.826           12724         12.4         1.9         15         14         US-10-247-893-25         0.826           c12726         <	12713	12.4	1.9		14	US-10-247-893-10	0.826667
12716         12.4         1.9         15         14         US-10-247-893-16         0.826           12717         12.4         1.9         15         14         US-10-247-893-17         0.826           12718         12.4         1.9         15         14         US-10-247-893-18         0.826           12719         12.4         1.9         15         14         US-10-247-893-19         0.826           12720         12.4         1.9         15         14         US-10-247-893-20         0.826           12721         12.4         1.9         15         14         US-10-247-893-21         0.826           12722         12.4         1.9         15         14         US-10-247-893-21         0.826           12723         12.4         1.9         15         14         US-10-247-893-21         0.826           12724         12.4         1.9         15         14         US-10-247-893-22         0.826           12725         12.4         1.9         15         14         US-10-247-893-23         0.826           c12726         12.4         1.9         15         14         US-10-247-893-25         0.826           c12727	12714	12.4	1.9	15	14	US-10-247-893-14	0.826667
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12721         12.4         1.9         15         14         US-10-247-893-21         0.826           12722         12.4         1.9         15         14         US-10-247-893-22         0.826           12723         12.4         1.9         15         14         US-10-247-893-23         0.826           12724         12.4         1.9         15         14         US-10-247-893-24         0.826           12725         12.4         1.9         15         14         US-10-247-893-25         0.826           c12726         12.4         1.9         15         14         US-10-248-18-4         0.826           c12727         12.4         1.9         15         14         US-10-294-203-4         0.826           c12728         12.4         1.9         15         15         US-10-440-850-111         0.826           c2046         14         2.1         17         14         US-10-338-777-231         0.825           c6553         13         1.9         16         15         US-10-297-068-870         0.8           c2511         13.8         2.1         17         9         US-09-866-108-7743         0.81           c2512         1	12719	12.4	1.9	15	14	US-10-247-893-19	0.826667
12722         12.4         1.9         15         14         US-10-247-893-22         0.826           12723         12.4         1.9         15         14         US-10-247-893-23         0.826           12724         12.4         1.9         15         14         US-10-247-893-24         0.826           12725         12.4         1.9         15         14         US-10-247-893-25         0.826           c12726         12.4         1.9         15         14         US-10-24818-4         0.826           c12727         12.4         1.9         15         14         US-10-294-203-4         0.826           c12728         12.4         1.9         15         15         US-10-440-850-111         0.826           c2046         14         2.1         17         14         US-10-338-777-231         0.826           c6553         13         1.9         16         15         US-10-297-068-870         0.8           c2511         13.8         2.1         17         9         US-09-866-108-7743         0.81°           c2512         13.8         2.1         17         9         US-09-866-108-7744         0.81°	12720	12.4	1.9	15	14	US-10-247-893-20	0.826667
12723         12.4         1.9         15         14 US-10-247-893-23         0.826           12724         12.4         1.9         15         14 US-10-247-893-24         0.826           12725         12.4         1.9         15         14 US-10-247-893-25         0.826           c12726         12.4         1.9         15         14 US-10-024-818-4         0.826           c12727         12.4         1.9         15         14 US-10-294-203-4         0.826           c12728         12.4         1.9         15         15 US-10-440-850-111         0.826           12729         12.4         1.9         15         15 US-10-444-347-28         0.826           c2046         14         2.1         17         14 US-10-338-777-231         0.826           c6553         13         1.9         16         15 US-10-297-068-870         0.8           c2511         13.8         2.1         17         9 US-09-866-108-7743         0.81           c2512         13.8         2.1         17         9 US-09-866-108-7744         0.81	12721	12.4	1.9	15	14	US-10-247-893-21	0.826667
12724         12.4         1.9         15         14         US-10-247-893-24         0.826           12725         12.4         1.9         15         14         US-10-247-893-25         0.826           c12726         12.4         1.9         15         14         US-10-024-818-4         0.826           c12727         12.4         1.9         15         14         US-10-294-203-4         0.826           c12728         12.4         1.9         15         15         US-10-440-850-111         0.826           c2046         14         2.1         17         14         US-10-338-777-231         0.826           c2546         14         2.1         17         14         US-10-297-068-870         0.826           c2511         13.8         2.1         17         9         US-09-866-108-7743         0.81           c2512         13.8         2.1         17         9         US-09-866-108-7744         0.81	12722	12.4	1.9	15	14	US-10-247-893-22	0.826667
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c12728         12.4         1.9         15         15 US-10-440-850-111         0.826           12729         12.4         1.9         15         15 US-10-444-347-28         0.826           c2046         14         2.1         17         14 US-10-338-777-231         0.826           c6553         13         1.9         16         15 US-10-297-068-870         0.8           c2511         13.8         2.1         17         9 US-09-866-108-7743         0.81           c2512         13.8         2.1         17         9 US-09-866-108-7744         0.81	c12726	12.4	1.9	15	14	US-10-024-818-4	0.826667
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45: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:* 46: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:* 47: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
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40. /CUIIZ Q/DIQUAId/Z/DIIA/USTUZD COIVID.SEU
<u> </u>
49: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*
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É.

	74: /cgn2_6					
	75: /cgn2_6	i/ptodata/2/	pna/US601	9_COMB.s	eq:*	
	76: /cgn2_6					
•	77: /cgn2_6	/ptodata/2	pna/US602	1_COMB.s	eq:*	
	78: /cgn2_6	/ptodata/2	pna/US602	2_COMB.s	eq:*	
	79: /cgn2_6	/ptodata/2	pna/US602	3A COMB.	.seq:*	
	80: /cgn2_6	/ptodata/2/	pna/US602	3B COMB.	.seq:*	
	81: /cgn2_6					
	B2: /cgn2_6					
	83: /cgn2_6		<u> </u>			
	84: /cgn2 6					
*****	85: /cgn2_6	_ •	•		<b>-</b>	
	86: /cgn2_6	<del></del>	<del></del>	<del></del>	<del>`</del>	
	87: /cgn2_6		·			
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	89: /cgn2_6		·		<del>.</del>	
	90: /cgn2_6		<u></u>		-	
	91: /cgn2_6					
	92: /cgn2_6	•	•	<del></del>		
	93: /cgn2_6	<u> </u>	•			
	94: /cgn2_6					
	95: /cgn2_6	<del></del>	·			
	96: /cgn2_6		*			
	97: /cgn2_6		•		<del>`</del>	
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	99: /cgn2_6					
	100: /cgn2_					
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	102: /cgn2_					
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	104: /cgn2_	· ·				
	105: /cgn2_				<u>-</u>	
	106: /cgn2_	6/ptodata/2	2/pna/US60	49_COMB.	seq:*	
	107: /cgn2_	<u> </u>				
-	108: /cgn2_	6/ptodata/2	2/pna/US60	51_COMB.	seq:*	
•	109: /cgn2_	6/ptodata/2	2/pna/US60	52_COMB.	seq:*	
•	110: /cgn2_	6/ptodata/2	2/pna/US60	53_COMB.	seq:*	
Pred. N	lo. is the nu	mber of res	sults predict	ed by chan	ce to have a	
					being printed,	
	derived by a					
		•				
	L	SUMMAR	IES			
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
c 667	17	2.5	17	ΛQ	US-10-293-338-3956	1, 1
28201	14	2.3	17		US-08-168-920E-45	0.933333
16424	14.4	2.1	16		US-09-528-209A-1600	0.9
c16425	14.4	2.1	16	48	US-10-287-822-789	0.9

16426	44.4	2.4	16	40	US-10-287-822-790	0.1
16426 c16427	14.4 14.4	2.1 2.1	16 16		US-10-287-822-791	0.9
	14.4	2.1	16		US-10-287-822-4210	0.
c16428 16429		2.1	16			
	14.4				US-10-287-822-4211	0.
c16430	14.4	2.1	16		US-10-287-822A-789	0.
16431	14.4	2.1	16		US-10-287-822A-790	0.
c16432	14.4	2.1	16		US-10-287-822A-791	0.
c16433	14.4	2.1	16		US-10-287-822A-4210	0.
16434	14.4	2.1	16		US-10-287-822A-4211	0.
c63801	13.4	2	15		PCT-US02-25942-3193	0.89333
c63802	13.4	2	15		PCT-US02-25942-3705	0.89333
c63803	13.4	2	15		PCT-US02-25943-41284	0.89333
63804	13.4	2	15	17	US-09-274-553-2507	0.89333
63805	13.4	2	15	17	US-09-274-553B-1174	0.89333
63806	13.4	2	15	17	US-09-274-553C-1174	0.89333
63807	13.4	2	15	17	US-09-274-553D-1174	0.89333
63808	13.4	2	15	17	US-09-274-553E-1174	0.89333
63809	13.4	2	15	21	US-09-504-231A-1174	0.89333
63810	13.4	2	15	21	US-09-504-231B-1174	0.89333
63811	13.4	2	15	25	US-09-611-931-1174	0.89333
63812	13.4	2	15	25	US-09-611-931A-1174	0.89333
c63813	13.4	2	15	47	US-10-227-565-41284	0.89333
c63814	13.4	2	15		US-10-227-567-3193	0.89333
c63815	13.4	2	15		US-10-227-567-3705	0.89333
c63816	13.4	2	15		US-10-303-778-1347	0.89333
c63817	13.4	2	15		US-10-305-274-95	0.89333
c63818	13.4	2	15		US-10-305-274-327	0.89333
63819	13.4	2	15		US-10-310-188-60805	0.89333
c63820	13.4	2	15		US-10-316-958-71	0.89333
c63821	13.4	2	15		US-10-367-729A-3193	0.89333
c63822	13.4	2	15		US-10-367-729A-3705	0.89333
c63823	13.4	2	15		US-10-367-832A-41284	0.89333
7875	15	2.2	17		US-10-310-188-60931	0.88235
28202	14	2.2	16		US-10-310-168-60931	0.86233
c 3	21.8	3.3	25		US-10-719-900-746277	0.87
c 4	21.8	3.3	25			
					US-60-427-808-746277	0.87
4786	15.4	2.3	18		US-10-310-188-28689	0.85555
16435	14.4	2.1	17		US-09-730-289B-27	0.84705
16436	14.4	2.1	17		US-10-061-077-79	0.84705
16437	14.4	2.1	17		US-10-061-077-80	0.84705
c16438	14.4	2.1	17		US-10-230-006-50	0.84705
c16439	14.4	2.1	17		US-10-230-006-547	0.84705
16440	14.4	2.1	. 17		US-10-300-683-252	0.84705
16441	14.4	2.1	17		US-10-310-188-24680	0.84705
16442	14.4	2.1	17		US-10-310-188-60661	0.84705
	14.4	2.1	17	52	US-10-471-271-4464	0.84705
c16443 c16444	17.7		17		US-10-471-271-4734	

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model March 29, 2004, 16:45:00; Search time 101.23 Seconds Run on: (without alignments) 4020.727 Million cell updates/sec US-09-477-082-1 Title: Perfect score: 670 Sequence: 1 aagcgctccaagacacgatt......ggggttaaataaagcgcttt 670 Scoring table: IDENTITY\_NUC Gapop 10.0, Gapext 1.0 1268986 segs, 303744313 residues Searched: 956702 Total number of hits satisfying chosen parameters: Minimum DB seq length: 15 Maximum DB seq length: 40 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 65000 summaries Pending\_Patents\_NA\_New:\* Database: 1: /cgn2 6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\* 2: /cgn2 6/ptodata/1/pna/US06\_NEW\_COMB.seq:\* 3: /cgn2 6/ptodata/1/pna/US07 NEW COMB.seq:\* 4: /cgn2 6/ptodata/1/pna/US08\_NEW\_COMB.seq:\* 5: /cgn2 6/ptodata/1/pna/US09\_NEW\_COMB.seq:\* 6: /cgn2 6/ptodata/1/pna/US10\_NEW\_COMB.seq:\* 7: /cgn2 6/ptodata/1/pna/US60 NEW\_COMB.seq:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. **SUMMARIES** % Result Query S/L DB Match Length No. Score 16 6 US-10-607-077A-43 0.8 4525 12.8 1.9 8.0 6 US-10-708-204-5066 c4526 12.8 1.9 16 0.79 1 PCT-US04-04452-1157 c 58 15.8 2.4 20 2.2 19 5 US-09-646-399A-3 0.789474 203 15

16466	11.8	1.8	15	6	US-10-781-758-5	0.786667
16467	11.8	1.8	15	6	US-10-045-674A-622	0.786667
16468	11.8	1.8	15	6	US-10-785-116-5	0.786667
169	15.2	2.3	20	6	US-10-780-439-41	0.76
170	15.2	2.3	20	6	US-10-690-276-106	0.76
171	15.2	2.3	20	6	US-10-690-276-107	0.76
4527	12.8	1.9	17	1	PCT-US03-27118-12	0.752941
59	15.8	2.4	21		PCT-US04-00035-9257	0.752381
16469	11.8	1.8	16		US-10-776-099-9	0.7375
c16470	11.8	1.8	16	6	US-10-398-483-10	0.7375
119	15.4	2.3	21		US-10-470-700A-36	0.733333
2815	13.2	2	18		PCT-US04-04452-905	0.733333
7644	12.4	1.9	17		US-09-941-492A-16	0.729412
1146	13.8	2.1	19		US-10-708-204-4501	0.726316
1147	13.8	2.1	19		US-10-664-668-42	0.726316
c1148	13.8	2.1	19		US-10-664-668-469	0.726316
1149	13.8	2.1	19		US-10-665-951-42	0.726316
c1150	13.8	2.1	19		US-10-665-951-469	0.726316
c1151	13.8	2.1	19		US-10-444-925A-309	0.726316
c 172	15.2	2.3	21		PCT-US04-00035-17210	0.72381
c52331	10.8	1.6	15		PCT-US04-07220-7	0.72
c52332	10.8	1.6	15		US-10-792-374-28	0.72
2	17.8	2.7	25		US-60-545-213-161396	0.712
c4528	12.8	1.9	18		US-10-021-698A-6079	0.71111
c 708	14.2	2.1	20		US-09-970-851-5	0.71
c12939	12	1.8	17		PCT-US03-31862-879	0.705882
12940	12	1.8	17		PCT-US03-31862-880	0.705882
12941	12	1.8	17		PCT-US03-25614-312	0.705882
12942	12	1.8	17		PCT-US03-25614-668	0.705882
c12943	12	1.8	17		US-10-488-588-9	0.705882
c 292	14.8	2.2	21		PCT-US04-00035-12137	0.704762
c 293	14.8	2.2	21		PCT-US04-00035-16634	0.704762
c 294	14.8	2.2	21		PCT-US04-00035-17209	0.704762
c 295	14.8	2.2	21		US-10-770-726-6140	0.704762
c 296	14.8	2.2	21		US-10-770-726-6141	0.704762
c 297	14.8	2.2	21		US-10-770-726-6143	0.704762
c 298	14.8	2.2	21		US-10-770-726-7109	0.704762
c 299	14.8	2.2	21		US-10-770-726-7110	0.704762
300	14.8	2.2	21		US-10-786-720-13106	0.704762
904	14.0	2.1	20		PCT-US04-04452-1268	0.704702
32789	11.2	1.7	16		US-10-796-280-68262	
c 354						0.7
355	14.6	2.2	21		PCT-US04-00035-8051	0.695238
356	14.6		21		PCT-US04-00035-54837 US-10-770-726-3594	0.695238
357	14.6	2.2	21			0.695238
	14.6	2.2	21		US-10-770-726-8593	0.695238
358	14.6	2.2	21		US-10-770-726-8779	0.695238
359	14.6	2.2	21		US-10-770-726-9390	0.695238
360	14.6	2.2	21		US-10-770-726-18917	0.695238
361	14.6	2.2	21	6	US-10-770-726-18918	0.695238

		nCore versi				
ļ	Copyright	(c) 1993 - 2	004 Comp	ugen Ltd.		
				-		
OM nucleic -	nuoloio o	oorob usin	a au madal			
OW HUCIER	· Hucleic S	earch, usin	g sw model			
Run on:	March 2	9 2004 13	·22·59 · Sea	rch time 18	394.17 Seco	nds
T Carr on:	101010112		out alignmer			
			2.735 Million		es/sec	
Title: L	JS-09-477	-082-1				
Perfect score	e: 670					
Sequence:	1 aagc	gctccaagac	acgatt	ggggttaaa	taaagcgcttt (	370
Scoring table					·	
G	apop 10.0	, Gapext 1	.0			
	075400		00400070			
Searched:	2/5132	ซษ seqs, 14	931090276	residues		
Total number	r of hite e	aticfying ch	ocon param	otore: 7	8694	
Total Hullibe	1 01 11115 5	alisiying cii	USEII Palaili	icicis. I	0094	
Minimum DE	3 sea lena	th: 15				
Maximum D						
IVIAXIII IAII B	D Joq long	g 10				
Post-process	sina: Minii	mum Match	0%			
· · · · · · · · · · · · · · · · · · ·		Match 100%				
		65000 sum				
	<u>_</u>					
Database :						
1:	em_estb	a:*				
	em_esth				*	
	em_estir					
	em_estn					
	em_esto					
	em_estp					
	em_estr					
	em_htc:					
	gb_est1:					
	): gb_est2					
	l: gb_htc:					
	2: gb_est3 3: gb_est4					
	s. gb_est					
	: gb_est					
	6: em_est			-		
	7: em_gs:					
	B: em_gs:					
	9: em_gs:					
	D: em_gs:					
	l: em_gs					
	2: em_gs:					
		.=	L	· <u></u>	·	

2	23: em_gss	mus:*				Ī
	24: em_gss					
2	25: em_gss	_rod:*				
	26: em_gss					
	27: em_gss					
	28: gb_gss			- , ,,, ,,,,		
	29: gb_gss2					
Pred. N	lo. is the nu	mber of res	sults predict	ed by chan	ce to have a	1
					being printe	
	derived by a					
		•				
	· · · · · · · · · · · · · · · · · · ·	SUMMAR	IES			
		%				
Result		Query				
No.	Score	Match	Length	DB	ID	S/L
			<u>-</u>			
c7143	11.8	1.8	15	10	BE230585	0.786667
7144	11.8	1.8	15		BQ582543	0.786667
7145	11.8	1.8	15		BQ585820	0.786667
7146	11.8	1.8	15		BQ590410	0.786667
7147	11.8	1.8	15		BQ590656	0.786667
7148	11.8	1.8	15		BQ591170	0.786667
7149	11.8	1.8	15		BQ591178	0.786667
7150	11.8	1.8	15		BQ591223	0.786667
7151	11.8	1.8	15		BQ594689	0.786667
7152	11.8	1.8	15		CF277319	0.786667
7153	11.8	1.8	15		CF281923	0.786667
7154	11.8	1.8	15		CF290920	0.786667
7155	11.8	1.8	15		CF291029	0.786667
7156	11.8	1.8	15		CF291103	0.786667
7157	11.8	1.8	15		CF291717	0.786667
7158	11.8	1.8	15		CF291798	0.786667
7159	11.8	1.8	15		CF292458	0.786667
7160	11.8	1.8	15		CF292461	0.786667
7161	11.8	1.8	15		CF298148	0.786667
7162	11.8	1.8	15		CF298630	0.786667
7163	11.8	1.8	15		CF298733	0.786667
7164	11.8	1.8	15		CF298805	0.786667
7165	11.8	1.8	15		CF298889	0.786667
7166	11.8	1.8	15		CF299602	0.786667
7167	11.8	1.8	15		CF299608	0.786667
7168	11.8	1.8	15		CF300121	0.786667
7169	11.8	1.8	15		CF300361	0.786667
7170	11.8	1.8	15		CF300992	0.786667
7171	11.8	1.8	15		CF302034	0.786667
7172	11.8	1.8	15		CF302124	0.786667
7173	11.8	1.8	15		CF302182	0.786667
7174	11.8	1.8	15		CF307923	0.786667
/ 1/7	11.0	1.0	13		0. 00/020	3.730007

Ge	nCore vers	ion 5.1.6			
Copyright	(c) 1993 - 2	004 Comp	ugen Ltd.		
OM nucleic - nucleic s	search, usin	g sw model			
Run on: March 2				004.06 Seco	nds
		out alignme			
,	1086	4.389 Millio	n cell upda	tes/sec	
Title: US-09-477	7-082-2				
Perfect score: 753		1	4		
Sequence: 1 aatta	igaccgcgtat	igaaa	.tacactggttt ⊤	tttaacctt 753	
Scoring table: IDENT	ITV NIIC				
Gapop 10.0		^		1	
Зарор то.	, Gapeki i	.0			
Searched: 347027	72 seqs, 216	1 371516995 i	residues		
Octronica. 047027			OSIGGOS		
Total number of hits s	atisfving ch	osen param	ieters: 1	364278	
				T T	
Minimum DB seq leng	th: 15				
Maximum DB seq len					
Post-processing: Mini	mum Match	0%			
Maximum	Match 100%	6			
Listing first	65000 sum	maries	·		
Database : GenEr					
1: gb_ba:*					
2: gb_htg:*					
3: gb_in:*				ļ	
4: gb_om:*					
5: gb_ov:*		, ,		-	
6: gb_pat:* 7: gb_ph:*					
7. gb_pii. 8: gb_pi:*					
9: gb_pr:*					
10: gb_ro:*					
11: gb_sts:					
12: gb_sy:					
13: gb_un:					
14: gb_vi:*					
15: em ba					
16: em_fur					
17: em_hu					
18: em_in:		-			
10. 0111 1111		<del> </del>	<del> </del>	1	
19: em_mi	J: <b>*</b>				
19: em_mı	1:*				

	7	*				
	3: em_pat:			<del></del>		
	4: em_ph:	•				
	5: em_pl:*					
	6: em_ro:*					-
	7: em_sts:					
	8: em_un:'	•				
	9: em_vi:*					
	0: em_htg_					
3	1: em_htg_	_inv:*	•			
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Result		Query				
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	1				 	
4757	14	1.9	15	6	AR231294	0.933333
c3023	14.4	1.9	16		A36563	0.933333
						0.9
3024	14.4	1.9	16		AR002257	1
3025	14.4	1.9	16		AR045207	0.9
3026	14.4	1.9	16		AR051238	0.9
c3027	14.4	1.9	16		AR087164	0.9
c3028	14.4	1.9	16		AR150597	0.9
c3029	14.4	1.9	16		E36063	0.9
3030	14.4	1.9	16		116032	0.9
3031	14.4	1.9	16		128367	0.9
c3032	14.4	1.9	16		142181	0.9
c3033	14.4	1.9	16		142187	0.9
c3034	14.4	1.9	16		149619	0.9
c3035	14.4	1.9	16	6	AR200478	0.9
c3036	14.4	1.9	16	6	AR371265	0.9
8238	13.4	1.8	15	6	AR029856	0.893333
c8239	13.4	1.8	15		AR029872	0.893333
8240	13.4	1.8	15		AR056159	0.893333
8241	13.4	1.8	15		AR056160	0.893333
0271	10.4	1.0	1.5		,	0.00000

	Co	nCore version	n F 1 G			
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OM pucloio	nuclaic s	earch, using	sw model			
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Bup on:	March 2	9 2004 11:	54·58 · Ses	rch time 32	5.436 Secon	nds ehr
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		, Gapext 1.	0			
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Searched:	337386	3 seqs, 212	4099041 re	sidues		
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Total numb	er of hits s	atisfying cho	sen param	eters: 20	072792	
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6	21	2.8	21	3	AAA51822	1
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120	18	2.4	20		ADE43355	0.9
3730	14.4	1.9	16		AAQ20008	0.9
3731	14.4	1.9	16		AAX18362	0.9
10799	13.4	1.8	15	2	AAQ21631	0.893333
10800	13.4	1.8	15	2	AAT00438	0.893333
10801	13.4	1.8	15	2	AAT52140	0.893333
10802	13.4	1.8	15	2	AAT52142	0.893333
10803	13.4	1.8	15	2	AAX14658	0.893333
c10804	13.4	1.8	15	2	AAX14674	0.893333
10805	13.4	1.8	15	5	AAA91455	0.893333
10806	13.4	1.8	15	5		0.893333
c10807	13.4	1.8	15	6		0.893333
10808	13.4	1.8	15	6	ABK81789	0.893333
c10809	13.4	1.8	15	7	ABZ66579	0.893333
c2080	15	2	17	9	ADE25221	0.882353
5799	14	1.9	16	2	AAX61143	0.875
15897	13	1.7	15	3	AAZ59262	0.866667
15898	13	1.7	15	4	AAF81549	0.866667
15899	13	1.7	15	4	AAF49044	0.866667
15900	13	1.7	15	4	AAF49043	0.866667
15901	13	1.7	15	4	AAF49042	0.866667
15902	13	1.7	15	5	AAH23587	0.866667
15903	13	1.7	15	6	ABA97405	0.866667
c15904	13	1.7	15	6	ABK72352	0.866667
15905	13	1.7	15	6	ABK98166	0.866667
15906	13	1.7	15	6	ABK98185	0.866667
15907	13	1.7	15	7	AAD47757	0.866667
15908	13	1.7	15	8	ADB68522	0.866667
8868	13.6	1.8	16	4	AAF82119	0.85
8869	13.6	1.8	16	5	AAH27758	0.85
8870	13.6	1.8	16	6	AAD44149	0.85
126	17.8	2.4	21	3	AAA51818	0.847619
3732	14.4	1.9	17	2	AAQ20006	0.847059
3733	14.4	1.9	17	2	AAQ20005	0.847059
3734	14.4	1.9	17	2	AAX69798	0.847059
3735	14.4	1.9	17	2	AAX69799	0.847059
3736	14.4	1.9	17	4	AAS06654	0.847059
c3737	14.4	1.9	17	7	ACC51390	0.847059
c3738	14.4	1.9	17	7	ACC51389	0.847059
c3739	14.4	1.9	17	7	ABT38540	0.847059
c3740	14.4	1.9	17	7	ADB05248	0.847059
c3741	14.4	1.9	17	7	ADB05249	0.847059
c3742	14.4	1.9	17	9	ADB42730	0.847059
c 324	16.8	2.2	20		ABZ77240	0.84
23979	12.6	1.7	15		AAA47676	0.84
23980	12.6	1.7	15		ABK46570	0.84
c23981	12.6	1.7	15		AAD26136	0.84
c23982	12.6	1.7	15		ABL91829	0.84
10810	13.4	1.8	16		AAT75139	0.8375
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Pred N	lo is the nu	mher of res	sults predict	ed by chan	ce to have a	
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		SUMMAR	IFS			<u> </u>
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Result		Query				
No.	Score	Match	Length	DB	ID	S/L
						<del></del>
2820	14	1.9	15	3	US-08-832-021-28	0.933333
2821	14	1.9			US-08-275-951-31	0.933333
1801	14.4	1.9		<u> </u>	US-08-087-387-6	0.9
1802	14.4	1.9			US-08-455-627-6	0.9
c1803	14.4	1.9			US-08-283-591-16	0.9
c1804	14.4				US-08-283-591-25	0.9
C10U4	14.4	1.9	10	l	03-06-263-391-23	0.8



c1805	14.4	1.9	16	1	US-08-088-658-34	0.9
1806	14.4	1.9	16	1	US-08-461-271-6	0.9
1807	14.4	1.9	16	1	US-08-713-685A-6	0.9
1808	14.4	1.9	16	2	US-08-689-856-6	0.9
c1809	14.4	1.9	16	2	US-08-471-907A-34	0.9
1810	14.4	1.9	16	. 3	US-09-070-477-6	0.9
c1811	14.4	1.9	16	3	US-08-088-661F-9	0.9
c1812	14.4	1.9	16	4	US-08-150-156A-21	0.9
c1813	14.4	1.9	16	. 4	US-08-108-591B-1	0.9
4872	13.4	1.8	15	1	US-08-425-315-1	0.893333
4873	13.4	1.8	15	2	US-08-292-620A-363	0.893333
4874	13.4	1.8	15	2	US-08-292-620A-364	0.893333
4875	13.4	1.8	15	2	US-08-173-489C-45	0.893333
ç4876	13.4	1.8	15	2	US-08-173-489C-61	0.893333
4877	13.4	1.8	15	3	US-08-716-190-11	0.893333
4878	13.4	1.8	15	3	US-08-832-021-24	0.893333
4879	13.4	1.8	15	3	US-08-832-021-54	0.893333
4880	13.4	1.8	15	3	US-09-071-845-363	0.893333
4881	13.4	1.8	15	3	US-09-071-845-364	0.893333
2822	14	1.9	16	4	US-09-531-000-9	0.875
7116	13	1.7	15	3	US-08-832-021-25	0.866667
7117	13	1.7	15	3	US-08-832-021-26	0.866667
7118	13	1.7	15	3	US-08-832-021-27	0.866667
1814	14.4	1.9	17	4	US-08-584-040-2548	0.847059
1815	14.4	1.9	17	4	US-08-584-040-2549	0.847059
1816	14.4	1.9	17	4	US-09-371-772B-1072	0.847059
1817	14.4	1.9	17	4	US-09-371-772B-1073	0.847059
4882	13.4	1.8	16	4	US-09-124-238A-4	0.8375
4883	13.4	1.8	16	4	US-09-331-930A-4	0.8375
4884	13.4	1.8	16	4	US-09-721-975-4	0.8375
4885	13.4	1.8	16	4	US-08-894-251A-5	0.8375
4886	13.4	1.8	16	4	US-09-300-958A-56	0.8375
4887	13.4	1.8	16	4	US-09-300-958A-83	0.8375
4888	13.4	1.8	16		US-09-986-621-4	0.8375
4889	13.4	1.8	16	·	US-09-527-972-15	0.8375
12749	12.4		15		US-08-087-387-5	0.826667
12750	12.4		15	L	US-08-455-627-5	0.826667
c12751	12.4		15		US-08-452-196A-6	0.826667
12752	12.4	1.6	15		US-07-971-978-1	0.826667
12753	12,4	1.6	15		US-08-461-271-5	0.826667
12754	12.4	1.6	15	L	US-08-713-685A-5	0.826667
c12755	12.4	1.6	15		US-08-756-728A-2	0.826667
12756	12.4		15		US-08-663-918-3	0.826667
c12757	12.4		15		US-08-663-918-4	0.826667
12758	12.4		15		US-08-689-856-5	0.826667
12759	12.4		15		US-08-292-620A-9	0.826667
12760	12.4		15		US-08-292-620A-360	0.826667
12761	12.4		15		US-08-292-620A-361	0.826667
12762	12.4	1.6	15	2	US-08-292-620A-362	0.826667

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M nucleic - nucleic search, using sw model	
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un on: March 29, 2004, 18:10:30 ; Search time 291.04 Seconds	
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9632.441 Million cell updates/sec	
itle: US-09-477-082-2	
Perfect score: 753	
equence: 1 aattagaccgcgtattgaaatacactggttttttaacctt 753	
3 3 3 3 3 3	
coring table: IDENTITY_NUC	
Gapop 10.0 , Gapext 1.0	
earched: 2458946 segs, 1861504846 residues	
otal number of hits satisfying chosen parameters: 1244038	
Minimum DB seq length: 15	
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Post-processing: Minimum Match 0%	
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Database : Published_Applications_NA:*	
1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*	
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*	
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*	
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*	
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*	
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*	
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*	
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score greater than or equal to the score of the result being printed,	
and is derived by analysis of the total score distribution.	

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		SUMMAR	lES			
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2297	. 14	1.9	15	14	US-10-188-404-31	0.933333
c1457	14.4	1.9	16	9	US-09-955-410-1	0.9
c1458	14.4	1.9	16	9	US-09-983-210-21	0.9
c1459	14.4	1.9	16	14	US-10-154-890-1	0.9
c4547	13.4	1.8	15	14	US-10-157-580A-142	0.893333
c 838	15	2	17	14	US-10-338-777-196	0.882353
7072	13	1.7	15	9	US-09-805-296D-12	0.866667
7073	13	1.7	15	14	US-10-072-975-12	0.866667
7074	13	1.7	15	14	US-10-051-436-12	0.866667
7075	13	1.7	15	15	US-10-360-275-12	0.866667
c 137	16.8	2.2	20	10	US-09-912-724-28	0.84
4548	13.4	1.8	16	9	US-09-811-093-21	0.8375
4549	13.4	1.8	16	9	US-09-777-422-11	0.8375
c4550	13.4	1.8	16	10	US-09-880-313A-42	0.8375
4551	13.4	1.8	16	10	US-09-997-672-30	0.8375
4552	13.4	1.8	16		US-09-986-625-4	0.8375
c4553	13.4	1.8	16	10	US-09-894-159-64	0.8375
4554	13.4	1.8	16	10	US-09-854-326-11	0.8375
4555	13.4	1.8	16	12	US-10-362-711-9	0.8375
4556	13.4	1.8	16	14	US-10-136-082-11	0.8375
4557	13.4	1.8	16	14	US-10-163-277-5	0.8375
4558	13.4	1.8	16	14	US-10-136-056-11	0.8375
4559	13.4	1.8	16	14	US-10-261-717-11	0.8375
4560	13.4	1.8	16	14	US-10-284-126-11	0.8375
4561	13.4	1.8	16	14	US-10-283-797-11	0.8375
4562	13.4	1.8	16	14	US-10-283-771-11	0.8375
4563	13.4	1.8	16	14	US-10-261-821-11	0.8375
c4564	13.4	1.8	16	14	US-10-164-915-2	0.8375
4565	13.4	1.8	16	14	US-10-262-258-11	0.8375
4566	13.4	1.8	16	14	US-10-262-264-11	0.8375
4567	13.4	1.8	16	14	US-10-262-252-11	0.8375
4568	13.4	1.8	16	14	US-10-261-787-11	0.8375
4569	13.4	1.8	16		US-10-176-812-5	0.8375
4570	13.4	1.8	16	14	US-10-135-671-11	0.8375
4571	13.4	1.8	16	14	US-10-176-549-5	0.8375
4572	13.4	1.8	16		US-10-292-951-4	0.8375
4573	13.4	1.8	16	14	US-10-431-304-15	0.8375
4574	13.4	1.8	16	14	US-10-283-874-11	0.8375
4575	13.4	1.8	16		US-10-362-262-3	0.8375
c14381	12.4	1.6	15		US-09-817-387-22	0.826667
14382	12.4	1.6	15		US-09-504-231A-22	0.826667
c14383	12.4	1.6	15		US-09-504-231A-1175	0.826667

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Searched:	375773	30 seqs, 17	593059518	3 residues			
				<u> </u>			
Total numbe	er of hits sa	atisfying ch	osen paran	neters: 2	26876998		
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N L Database : 1: 2: 3:	Aaximum Maximum Maximum Misting first  Pendin  /cgn2_6/ /cgn2_6/ /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:* na/PCTUS na/US06_0 na/US07_0	COMB.seq: COMB.seq:	k		•
N L Database : 1: 2: 3:	Aaximum Naximum Naximu	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:*  NA_Main:* na/PCTUS na/US06_0 na/US07_0 na/US080_	_COMB.seq: COMB.seq: COMB.seq: COMB.seq	*		,
N L Database : 1: 2: 3: 4: 5:	Alaximum Maximum Maxim	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	maries NA_Main:* na/PCTUS na/US06_C na/US07_C na/US080_ na/US081_	_COMB.seq: COMB.seq: COMB.seq COMB.seq	* : * : *		•
N L Database : 1: 2: 3: 4: 5:	Pendin /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	maries NA_Main:* na/PCTUS na/US06_0 na/US07_0 na/US080_ na/US081_ na/US082_	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq	**		
N L Database : 1: 2: 3: 4: 5: 6: 7:	Alaximum Maximum Maximum Misting first  Pendin  /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:* NA_Main:* na/PCTUS na/US06_0 na/US07_0 na/US080_ na/US081_ na/US082_ na/US083	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq	* * * * * * * * * * * * * * * * * * *		
N L Database : 1: 2: 3: 4: 5: 6: 7:	Alaximum Maximum Maximum Misting first  Pendin  /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/ /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:* NA_Main:* na/PCTUS na/US06_0 na/US07_0 na/US080_ na/US081_ na/US082_ na/US083	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq	* * * * * * * * * * * * * * * * * * *		*
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9:	Pendin / /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:* NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US082_ na/US083_ na/US084_ na/US085_	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq	* * * * * * * * * * * * * * * * * * * *		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9:	Pendin / /cgn2_6/	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	MA_Main:* NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US082_ na/US083_ na/US084_ na/US085_	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq	* * * * * * * * * * * * * * * * * * * *		•
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9:	### Alaximum Naximum N	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	maries NA_Main:* na/PCTUS na/US06_C na/US080_ na/US081_ na/US082_ na/US083_ na/US084_ na/US085_ pna/US086	COMB.seq: COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq	:* :* :* :* :* :* q:*		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9:	Pendin   Pendin   /cgn2_6/   /cgn	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p	maries NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US082_ na/US083_ na/US084_ na/US085_ pna/US086	COMB.seq: COMB.seq: COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq COMB.seq	:* :* :* :* :* :* q:* q:*		
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N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10	### Alaximum Naximum N	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085 pna/US0888 pna/US0888	COMB.seq: COMB.s	* :* :* :* :* :* :* :* :* :* :* :* :* :*		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12	Alaximum Maximum Maxim	Match 100% 65000 sum g_Patents_ ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/p ptodata/2/ b/ptodata/2/ b/ptodata/2/ b/ptodata/2/ b/ptodata/2/	maries  NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085 pna/US0889 pna/US0889 pna/US089	COMB.seq: COMB.s	* :* :* :* :* :* :* :* q:* q:* q:* q:* q		*
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13	Alaximum Maximum Maxim	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_C na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086	COMB.seq: COMB.s	* :* :* :* :* :* :* q:* q:* q:* q:* q:*		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13	### Alaximum Maximum M	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085_ pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086 pna/US086	COMB.seq: COMB.s	* :* :* :* :* :* :* :* q:* q:* q:* q:* q		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13 14	### Alaximum Maximum M	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_0 na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085_ pna/US086 pna/US086 pna/US086 pna/US086 pna/US089 pna/US090 pna/US091 pna/US092	COMB.seq: COMB.s	* :* ::* ::* ::* ::* ::* ::* ::* ::* ::		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13 14 15 16	Alaximum Maximum Maxim	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_C na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085 pna/US086 pna/US0889 pna/US089 pna/US099 pna/US092 pna/US093	COMB.seq: COMB.s	* :* :* :* :* :* :* :* :* :* :* :* :* :*		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13 14 15 16	Alaximum Maximum Maximum Maximum Misting first  Pendin (cgn2_6/)	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p	maries  NA_Main:  na/PCTUS  na/US06_C  na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085 pna/US086 pna/US086 pna/US086 pna/US086 pna/US089 pna/US090 pna/US092 pna/US093	COMB.seq: COMB.s	* :* :* :* :* :* :* :* :* :* :* :* :* :*		
N L Database : 1: 2: 3: 4: 5: 6: 7: 8: 9: 10 11 12 13 14 15 16 17 18	Alaximum Maximum Maxim	Match 100% 65000 sum g_Patents_ ptodata/2/p p/ptodata/2/p	maries  NA_Main:* na/PCTUS na/US06_C na/US080_ na/US081_ na/US083_ na/US084_ na/US085_ pna/US085_ pna/US086 pna/US096 pna/US096	COMB.seq: COMB.s	* :* :* ::* ::* ::* ::* ::* ::* ::* ::*		

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	80: /cgn2_0	6/ptodata/2/	pna/US602	3B_COMB.	seq:*		
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	107: /cgn2_	_6/ptodata/2	2/pna/US60	50_COMB.	seq:*		
	108: /cgn2_	_6/ptodata/2	2/pna/US60	51_COMB.	seq:*		
	109: /cgn2	6/ptodata/2	2/pna/US60	52 COMB.	seq:*		
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6	21	2.8	21	20	US-09-477-082-33		1
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c 20	20		20		US-10-293-338-2237		1
				70			

c8917	15	2	15	1	PCT-US02-25944-4476	1
c8918	15	2	15		PCT-US02-25944-4488	1
c8919	15	2	15		US-10-227-564-4476	1
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31751	14	1.9	15		PCT-US02-25944-2473	0.933333
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c18620	14.4	1.9	16		US-10-287-787-25195	0.9
c2270	16	2.1	18		US-10-310-188-83566	0.888889
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5275	15.4	2	18		US-10-310-188-9840	0.855556
c5276	15.4	2	18	49	US-10-310-188-14825	0.855556

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OM nucleic	- nucleic si	earch, using	3 SW Model			
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Searched:	126898	6 seqs, 303	744313 res	dues		
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Result		Query				
No.	Score	Match	Length	DB	ID	S/L
28	16.8	2.2	20	6	US-10-690-276-174	0.84
2380	13.4			1	PCT-US04-07616-4	0.8375
8186	12.4				US-10-781-758-5	0.826667
8187	12.4		15		US-10-045-674A-622	0.826667
					US-10-456-982-8	0.826667

8189	12.4	1.6	15	6	US-10-785-116-5	0.826667
c1329	13.8	1.8	17		PCT-US03-25614-376	0.811765
285	15	2	19		US-10-708-204-5035	0.789474
17660	11.8	1.6	15		US-10-788-232-132	0.786667
8190	12.4	1.6	16		US-10-776-099-9	0.775
c8191	12.4	1.6	16		US-10-398-483-10	0.775
c 46	16.2	2.2	21		PCT-US04-00035-23548	0.771429
c 47	16.2	2.2	21		US-10-786-720-6011	0.771429
135	15.4	2	20		US-10-667-275A-7	0.77
195	15.2	2	20		PCT-US04-04205-2	0.76
196	15.2	2	20		PCT-US04-04452-770	0.76
197	15.2	2	20		US-10-777-838-2	0.76
198	15.2	2	20		US-10-789-113-3	0.76
199	15.2	2	20		US-10-789-113-4	0.76
c 200	15.2	2	20		US-10-476-021-97	0.76
4842	12.8	1.7	17		US-10-398-445-51	0.752941
807	14.2	1.9	19		PCT-US03-35072-23	0.747368
808	14.2	1.9	19		US-10-387-346B-154	0.747368
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810	14.2	1.9	19		US-10-664-668-600	0.747368
c 811	14.2	1.9	19		US-10-665-951-173	0.747368
812	14.2	1.9	19		US-10-665-951-600	0.747368
c17661	11.8	1.6	16		US-10-708-204-4602	0.7375
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1003	14	1.9	19		US-10-664-668-246	0.736842
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c 136	15.4	2	21		PCT-US04-00035-22644	0.733333
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8193	12.4	1.6	17		PCT-US03-31862-1340	0.729412
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201	15.2	2	21		PCT-US04-00035-2986	0.72381
202	15.2	2	21		PCT-US04-00035-9540	0.72381
203	15.2	2	21		PCT-US04-00035-9756	0.72381
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205	15.2	2	21		PCT-US04-00035-31098	0.72381
206	15.2	2	21		PCT-US04-00035-31101	0.72381
	10.2		21	• •		0.72001

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Minimum	DB seq leng	gth: 15				
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Post-proce	essing: Mini					
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Pred. No. is the number of results predicted by chance to have a										
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Result		Query								
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3024	14	1.9	15	10	AW246494	0.933333				
c4962	13	1.7	15		CF543203	0.866667				
c3920	13.4	1.8	16		CF291803	0.8375				
510	15.8	2.1	19		AZ645841	0.831579				
96	17.4	2.1	21		AZ647578	0.828571				
c6707	17.4	1.6	15		BE230585	0.826667				
6708	12.4	1.6	15		BQ582543	0.826667				
		1.6	15		BQ585820	0.826667				
6709 6710	12.4	1.6	15		BQ590410	0.826667				
	12.4									
6711	12.4	1.6	15		BQ590656	0.826667				
6712	12.4	1.6	15		BQ591170	0.826667				
6713	12.4	1.6	15		BQ591178	0.826667				
6714	12.4	1.6	15		BQ591223	0.826667				
6715	12.4	1.6	15		BQ594689	0.826667				
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c6718	12.4	1.6	15		CF290849	0.826667				
6719	12.4	1.6	15		CF290920	0.826667				
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6724	12.4	1.6	15		CF292458	0.826667				
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6732	12.4	1.6	15	14	CF298889	0.826667				
6733	12.4		15	14	CF299602	0.826667				

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FEATURES
source
Search completed: March 31, 2004, 14:14:07 Job time : 0.001 secs
                                                                                                                                                                                                                        Query Match 1.2%; Score 9.2; Best Local Similarity 78.6%; Pred. No. 0; Matches 11; Conservative 0; Mismatche
                                                                                                                                                  638 TGCCCAAAAAACAA 651
                                                                                                              15 TGATCAAAAAAAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: D column: 12

Plate: LLCM7 row: D column: 12

High quality sequence stop: 14.

Location/Qualifiers
1. .15
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol type="mrNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
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/cell line="MGC3"
/lab host="mulb (phage-resistant)"
/clone lib="NIH MGC_7"
/clone lib="NIH MGC_7"
/clone lib="NIH MGC_7"
/clone into EcoRI/XhoI sites using the following 5'
sadaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Minimum
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VERSION
KEYWORDS
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AW246494
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DEFINITION
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Maximum Match 100%
Listing first 100 summaries
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Pas
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information of the L.M.A.G.E.

Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center. Vec
                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_EST8: 2821595.5prime
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                          AW246494
2821595.3prime NIH_MGC_7
                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Copyright (c) 1993 - 2004 Compugen Ltd
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ACCESSION: AW246494
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AUTHORS
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AW246494/c
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                  AL Unpublished (1999)
Other ESTS: 2821595.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Tissue Procurement: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
scores: PHRED from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Genome Center
http://www.genome.washington.edu Low Quality Sequence: 14
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 15 contiguous distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at the beginning of the sequence, this cDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyadenylated
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   following vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_7"
/clone="Grgan: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/cnote="Gryan made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
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Pred. No.
sequence.
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B
         Polyadenylation: Based upon the
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Sequence 31, Application US/10188404

Publication No. US20030105286A1

GENERAL INFORMATION:
APPLICANT: Egholm, Michael
APPLICANT: Neilsen, Peter
APPLICANT: Neilsen, Ole
APPLICANT: Dueholm, Kim L.
APPLICANT: Coull, James M.
APPLICANT: Coull, James M.
APPLICANT: Kiely, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-09-983-210-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PATENTIN version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ş
               APPLICANT: Neilsen, Peter
APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Kim L.
APPLICANT: Christensen, Leif
APPLICANT: Christensen, Leif
APPLICANT: Coull, James M.
APPLICANT: Coull, James M.
APPLICANT: Griffith, Michael
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: 15155042
CURRENT APPLICATION NUMBER: US/10/188,404
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: 08/275,951
PRIOR FILING DATE: 1994-07-15
PRIOR FILING DATE: 1997-04-23
NUMBER OF SEQ ID NOS: 69
PRIOR FILING DATE: 1997-04-23
NUMBER: Date of the prior of th
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US-10-154-890-1
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APPLICANT: Begholm, Michael
APPLICANT: Mielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLS OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
CURRENT APPLICATION NUMBER: US/10/154,890
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/08/108,591
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3
Best Local Similarity 84.6
Matches 11; Conservative
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: No. US20030180734A1el Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 CCCAAAAACAAG 652
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; SEQ ID NO 31
; LENGTH: 15
; TYPEL DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
; LOCATION: (6), 7(7)
; COTHER INFORMATION: Amino Hexanoic Acid, Lysine,
; COTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
US-10-188-404-31

Query Match
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 10; Conservative 0; Mismatches 2; Indels 0;
Matches 10; Conservative 0; Mismatches 2; Indels 0;

Qy 18 AAAGTAAAAAAAA

Search completed: March 31, 2004, 14:11:57

Search completed: March 31, 2004, 14:11:57
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Gaps

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APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
CURRENT APPLICATION NUMBER: US/10/154,890
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US/08/108,591
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/275,951
PRIOR FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/765,798
PRIOR FILING DATE: 1997-04-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
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Best Local 2
                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/188,404
CURRENT FILING DATE: 2002-07-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Egholm, Michael
                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (6)..(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine,
OTHER INFORMATION: Amino Hexanoic Acid, Lysine Linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ISIS5042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Griffith, Michael IIILE OF INVENTION: Linked Peptide Nucleic Acids
                                                                                                                                                                                                                                                                                                                               LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: No. US20030180734A1el Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic construct FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                     Local
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1.9%; Score 14.4; DB 1; Length 16;
Local Similarity 93.8%; Pred. No. 1.2;
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                                                                                                     Similarity 100.0%;
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Buchardt, Ole
Dueholm, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Christensen, Leif Coull, James M.
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                                                                                   Conservative
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  ITCTTTT 15
                                   TCTTTT 473
                                                                                                   1.9%; Score 14; DB 1; Length 15; 00.0%; Pred. No. 1.5;
                                                                                   Mismatches
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                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nielsen, Peter Eigil
APPLICANT: Nielsen, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases
FILE REFERENCE: ISIS4800
CURRENT APPLICATION NUMBER: US/09/955,410
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR APPLICATION NUMBER: 09/686,114
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: 09/686,114
PRIOR FILING DATE: 1996-07-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                        APPLICATION NUMBER: N. CONTROL PRIOR APPLICATION DATA:

PRIOR APPLICATION UNMBER: DK 098

FILING DATE: 24-MAY-1991

PRIOR APPLICATION NUMBER: DK 051

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 051

FILING DATE: 15-APR-1992

INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
offen NUMBER: circle
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09955410 Patent No. US20020146718A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                           APPLICATION NUMBER: US 00
FILING DATE: 1994-APR-05
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 00
FILING DATE: 24-MAY-1991
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0:
FILING DATE: 2001-OCT-23
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TH
TITLE OF INVENTION: DI.
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
STRANDEDNESS:
TOPOLOGY: li:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640 CCCAAAAAACAAG 652
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US2002016038321
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linear
                 single
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84.6%;
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                                                                                                                                        DK 0510/92
                                                                                                                                                                                                        DK 0987/91
                                                                                                                                                                                                                                                                 DK 0986/91
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Pred. No. 6.
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MOLECULE TYPE:

DNA (genomic)

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Sequence 1. Application US/0995410

Patent No. US20020146718A1

Patent No. US20020146718A1

Patent No. US20020146718A1

PAPLICANT: Buchardt, Ole

APPLICANT: Egholm, Michael

APPLICANT: Berg, Rolf Henrik

TITLE OF INVENTION: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleobases

FILE REFERENCE: ISIG4800

CURRENT APPLICATION NUMBER: US/09/955,410

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 08/108,591

PRIOR APPLICATION NUMBER: 09/686,114

PRIOR FILING DATE: 1993-11-22

PRIOR FILING DATE: 1993-17-24

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.1
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US-09-955-410-1/c
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Maximum Match 100%
Listing first 50 summaries
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Maximum DB
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Perfect score:
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9.8
9.8
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seq length: 2000000000
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Match
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US-09-983-210-21

US-10-154-890-1

US-10-188-404-31

US-09-955-410-1

US-09-983-210-21

US-10-154-890-1

US-10-188-404-31
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Compugen Ltd.
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Sequence 21, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 31, Appli
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; ANTI-SENSE: NO
PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILLING DATE: 22-MAY-1992
US-09-983-210-21
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: Sequence 21, Application US/09983210

: Patent No. US20020160383A1
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                                                                        Query Match
Best Local :
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Best Local (
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INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/9
FILING DATE: 2001-OCT-23
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1
FILING DATE: 1994-APR-05
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                          TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-MAY-PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-MAY-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DK 0: FILING DATE: 24-MAY-1991
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                        715 CTTTTTTTTTTGATC 730
16
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15; Conserv
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                                                        Conservative
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E: DNA (genomic)
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 14.4;
93.8%; Pred. No. 1.
                                                                      1.9%; Score 14.4;
93.8%; Pred. No. 1
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CAL PROCEDURES
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RESULT 3
US-10-154-890-1/c
US-10-154-890-1/c
; Sequence 1, Application US/10154890
; Publication No. US20030180734A1
; GENERAL INFORMATION:

```
APPLICANT: Ducholm, Kim L.
APPLICANT: Christensen, Leif
TITLE OF INVENTION: Linked Peptide Nucleic Acids
FILE REFERENCE: ISLS1577
CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/08,591
PRIOR FILING DATE: 1993-11-22
PRIOR PRILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/088,661
PRIOR APPLICATION NUMBER: 95/91
PRIOR APPLICATION NUMBER: 95/91
PRIOR APPLICATION NUMBER: 986/91
PRIOR APPLICATION NUMBER: 986/91
PRIOR FILING DATE: 1991-05-22
PRIOR APPLICATION NUMBER: 987/91
PRIOR FILING DATE: 1991-05-24
PRIOR PRILING DATE: 1991-05-24
PRIOR PRILING DATE: 1991-05-24
PRIOR PRILING DATE: 1991-05-05-05
PRIOR FILING DATE: 1991-05-05-07
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US-08-275-951-31/c
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                                                                                                                                                           RESULT 30
US-08-832-021-28/c
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Best Local Similarity 90.9%;
Matches 10; Conservative
Sequence 28, Application US/08832021 Patent No. 6045998 GENERAL INFORMATION:
APPLICANT: Combates, N. APPLICANT: Pardinas, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Egholm,
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
NAME/KEY: misc_feature
LOCATION: (6)...(7)
OTHER INFORMATION: Lysine, Amino Hexanoic Acid, Lysine, Amino
OTHER INFORMATION: Hexanoic Acid, Lysine Linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Y Match 1.2%;
Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 AAAAAACAAGT 653
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Buchardt, Ole
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Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8.8; D
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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; OTHER INFORMATION: Description of Artificial Sequence: primer US-08-832-021-28
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                                                                                                                                                                                                                     APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
APPLICANT: Stenn, K.
TITLE OF INVENTION: IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
FILE REFERENCE: JBP-382
CURRENT APPLICATION UNMEER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
RUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
                                              Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                 642 CAAAAAACAA 651
3
CAAAAAAAAA
.
                                                                  0; Mismatches
                                                                                   Score 8.4;
Pred. No. 3
                                                                                                    DB 1; Length 15
                                                                    1; Indels
                                                                    0
                                                                  Gaps
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Search completed: March 31, 2004, 14:10:54 Job time : 0.001 secs

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                                                                                                                                                                                                                                             Patent No. 5830658
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,271
APPLICATION NUMBER: 08/087,387
FILING DATE:
APPLICATION NUMBER: 08/087,387
FILING DATE:
APPLICATION NUMBER: 08/087,387
FILING DATE:
APPLICATION NUMBER: 08/087,387
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 104
REFERENCE/DOCKET NUMBER: 104
REJECOMMUNICATION INFORMATION:
TELEPAX: (415) 358-785
TELEPAX: (415) 358-785
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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             ZIP: 94306-2155

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Oligonucleotide clamps having diagnostic TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Word for Windows, vers. 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,685A
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MEDIUM TYPE: 5.25 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM:
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  APPLICATION NUMBER:
                                                                                                                                                                      COUNTRY:
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o. 5830658
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T: 465 Lincoln Centre Drive
Foster City
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Five Palo Alto Square, 3000 El Camino Real
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US/08/689,856
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RESULT 28
US-09-070-477-6/c
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                       ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELEPHONE: (415) 358-7855
TELEPHONE: (415) 358-794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
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GENERAL INFORMATION:
APPLICANT: Sergei
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,477
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PRIOR APPLICATION NUMBER: US/08/455,627
PRILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STRIE: California
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LENGTH: 16 nucleotides
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Oligonucleotide clamps having diagnostic TITLE OF INVENTION: and therapeutic applications
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYN
BLECOMMUNICATION INFORMATION:
TELEPHONE: 415,843-5000
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                                                                                                                                                                                                                                  FILING DATE:
APPLICATION NUMBER: 08/461,271
FILING DATE:
APPLICATION NUMBER: 08/087,387
STRANDEDNESS:
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Pred. No. 26;
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                                 COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatable
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMULTA, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: 35,966
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000
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Best Local Similarity 90.9%;
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APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,387
FILING DATE: 19330702
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
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MEDIUM TYPE: 5.25 in
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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Five Palo Alto Square, 3000 El Camino Real
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Pred. No.
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RESULT 26 US-08-713-685A-6/c

Sequence 6, Application US/08713685A Patent No. 5817795 GENERAL INFORMATION:

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Patent No. 5741643
GENERAL INFORMATION:
                                                      Matches
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                                                                    Query Match
Best Local :
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                                                                                                                                                                                                TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,
FILING DATE: 2-011-93
ATTORNEY,AGENT INFORMATION:
NAME: Stephen C. Macevicz
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Oligonucleotide clamps having diagnostic TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          TOPOLOGY:
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                         643 AAAAAACAAGT 653
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10; Conserv
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F: 465 Lincoln Centre Drive
Foster City
California
                                                                  Similarity
                                                                                                                                                                                                              3: (415)
(415) 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                      Conservative
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                                                                    Score 9.4; I
Pred. No. 26;
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                                                      Mismatches
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US-08-150-156A-21
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CURRENT APPLICATION NUMBER: US/08/086,661F
CURRENT FILING DATE: 193-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                         Sequence 21, Application US/08150156A Patent No. 6357163
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local &
                                                                                                                                                                                                                                                         Patent No. 6357163
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24 MAY-1991
                                                                 SOPTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08.
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                      TITLE OF INVENTION: THE USE OF NUCLEIC ACID ANALOGUES IN TITLE OF INVENTION: DIAGNOSTICS AND ANALYTICAL PROCEDURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: r
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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Wittung, Pernilla
Buchardt, Ole
Egholm, Michael
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                                                                    US/08/150,156A
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Pred. No. 25;
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US-08-108-591B-1
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US-08-087-387-6/c
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APPLICANT: Buchardt, Ole
APPLICANT: Buchardt, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                           Sequence 6, Application US/08087387
Patent No. 5473060
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleol
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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Patent No. 6395474
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APPLICATION NUMBER: DK 0
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
             CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
CITY: Foster City
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                                                                  Oligonucleotide clamps having diagnostic andtherapeutic applic
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Pred. No. 25;
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RESULT 18
US-08-088-658-34
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COUNTY: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Release #1.0, Version #1
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5641625
GENERAL INFORMATION:
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/283,591
FILING DATE: N/A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     APPLICANT: M llegaard, Niels E.

ITTLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF

ITTLE OF INVENTION: NUCLEIC ACIDS
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ADDRESSEE: No. 5629152718
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                 STATE: F
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ZIP: 19103
                                                                                                                                                                                 STREET: One Liberty CITY: Philadelphia
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                                                                                                                                                                                                                       ADDRESSEE:
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EDNESS: single
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Berg, Rolf H.
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Egholm, Michael
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Pred. No. 25
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RESULT 19
US-08-471-907A-34
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GENERAL INFORMATION:
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Best Local S
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TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3
TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFFLICATION NUMBER: 08/054,363
FILING DATE: 26-APRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ":::::
                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,907A
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: Come Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                 NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: M llegaard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Out - CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: singi
TOPOLOGY: linear
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                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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Egholm, Michael
                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berg, Rolf H.
M llegaard, N
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                                      215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peter E.
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                                                                                                                                                                08/088,658
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                                                                      ISIS-1052
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US-08-832-021-28

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                                                                                    SOFTWARE: PA
SEQ ID NO 31
LENGTH: 15
TYPE: DNA
                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/088,61
PRIOR FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/088,61
PRIOR APPLICATION NUMBER: PCT/EP92.
PRIOR FILING DATE: 1993-07-02
PRIOR REPLICATION NUMBER: PCT/EP92.
PRIOR APPLICATION NUMBER: 986/91
PRIOR FILING DATE: 1991-05-22
PRIOR FILING DATE: 1991-05-22
PRIOR FILING DATE: 1991-05-24
PRIOR FILING DATE: 1991-05-25
PRIOR FILING DATE: 1991-05-27
PRIOR FILING DATE: 1991-05-24
PRIOR FILING DATE: 1991-05-24
PRIOR FILING DATE: 1991-05-24
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LENGTH: 15
TYPE: DNA
CRGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/275,951
CURRENT FILING DATE: 1994-07-15
PRIOR APPLICATION NUMBER: 08/108,591
PRIOR FILING DATE: 1993-11-22
PRIOR FILING DATE: 1993-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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CURRENT APPLICATION NUMBER: US/08/832,021
CURRENT FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Parimoo, S.
APPLICANT: Prouty, S.
APPLICANT: Stenn, K.
APPLICANT: SIEDN, IMPROVED TECHNIQUE FOR DIFFERENTIAL DISPLAY
                                                                                                                                                    NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Buchardt, Ole
APPLICANT: Dueholm, Kim L.
APPLICANT: Christensen, Leif
TITLE OF INVENTION: Linked Peptide Mucleic Acids
FILE REFERENCE: ISIS1577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atent No.
                                                             ORGANISM: Artificial Sequence
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                  THER INFORMATION: Description of Artificial Sequence: No. 6451968el Sequence
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5. 6045998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kiely, John
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RESULT 17
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                                                                                                          Query Match 1.3%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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Patent No. 56291
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Best Local Similarity
                                                                                                                                                                                                                                                                          TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
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APPLICANT: Raviku
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US
FILING DATE: N/A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6)..(7)
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 16
                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                          TYPE: nucleic acid
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ADDRESSEE: No. 5629152718
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                           EGISTRATION NUMBER:
                                                                             640 CCCAAAAAACAAG 652
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                                              4 CCAAAAAAAAAAG 16
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                                                                                                                                                                                         ss: single
linear
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                                                                                                                             Score 9.8; I
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                                                                                                              Mismatches
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                                                                                                                                           Length 16
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US-08-283-591-25

Sequence 25, Application US/08283591 Patent No. 5629152 GENERAL INFORMATION:

APPLICANT:

Ravikumar, Vasulinga

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RESULT 12
US-08-150-156A-21/c
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CURRENT APPLICATION NUMBER: US/08/08/661F
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOPTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: 1
Sequence 21, Application US/08150156A Patent No. 6357163
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THE USE OF NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 358-78
TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICATION NUMBER: 08/0
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
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Local Similarity 93.8%;
les 15; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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Wittung, Pernilla
Buchardt, Ole
Egholm, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9%; Score 14.4;
93.8%; Pred. No. 4.
           THE USE OF NUCLEIC ACID ANALOGUES IN DIAGNOSTICS AND ANALYTICAL PROCEDURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/087,387
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Pred. No. 4.
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                                                                                                                              , OTHER INFORMATION: No. 6395474el Sequence \ensuremath{\text{US-08-108-591B-1}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ANTI-SENSE: NO PUBLICATION INFORMATION: DOCUMENT NUMBER: WO PCT/EP92/01220 FILING DATE: 22-WAY-1992 US-08-150-156A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-108-591B-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DK 051
FILING DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
CTPNE: nucleic acid
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 16
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                  Matches
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Patent No. 6395474
                                                                                 Query Match
Best Local
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Best Local Similarity 93.8%;
                                                                                                                                                                                                                                                                                                                  APPLICANT: Buchardt, Ole
APPLICANT: Eigholm, Michael
APPLICANT: Nielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
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APPLICATION NUMBER: DK 0:
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                               Local
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                                 715
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                                                                  l Similarity
15; Conserv
                             CTTTTTTTTTTGATC 730
                                                                 Conservative
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                                                                               1.9%;
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                                                               Score 14.4; D
Pred. No. 4.3;
0; Mismatches
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Pred. No. 4.3;
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                                                                                                Length 16;
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NUMBER OF SEQUENCES:

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Best Local S
Matches 15
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 16 nucleotides
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                                                                                                                                            Sequence 34, Application US/08471907A Patent No. 5986053
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,856
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: NAMEMING. JAFFIEN
                                                                                                                              GENERAL
                                                                              APPLICANT: I
APPLICANT: I
APPLICANT: I
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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   OF INVENTION:
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CANT: Sergei M.
                                                                                                                              INFORMATION:
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Five Palo Alto Square, 3000 El Camino Real
Buchardt, Ole
Egholm, Michael
Nielsen, Peter E.
Berg, Rolf H.
M llegaard, Niels E.
MURITION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
NVENTION: NUCLEIC ACIDS
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                                                                                                                  Ecker, David J.
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                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6048974
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09070477 Patent No. 6048974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers.
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                            CLASSIFICATION: PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       STREET: 465 Lincoln Centre Drive CITY: Poster City STATE: California COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                  COUNTRY: USA
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9%; Score 14.4;
93.8%; Pred. No. 4
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08/461,271
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                              US/08/713,685
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US-08-461-271-6
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Patent No. 5741643
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonuclectide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: 08/054,363
PILING DATE: 26-APPLI-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCES/DOCKET NUMBER: ISIS-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/088,658
FILING DATE: 19930702
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TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th floor
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
COMPUTER: 5.05 inch diskette
COMPUTER: IEM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,271
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One Libert;
CITY: Philadelphia
                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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93.8%; Pred. No. 4.3;
active 0; Mismatches
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US-08-713-685A-6
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TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                         US-08-713-685A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08713685A
Patent No. 5817795
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Best Local :
Query Match
Best Local Similarity
                                                                                                                                                            TELEFAX: (415) 358-7794
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/087,38:
FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)358-7855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
APPLICATION NUMBER: 08
                                                                                                                                                                             REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION: (415) 358-7855
TELEPAX: (415) 358-7794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics
STREET: 465 Lincoln Centre Drive
CITY: Foster City
STATE: California
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Oligonucleotide clamps having diagnostic
TITLE OF INVENTION: and therapeutic applications
                                                                                                                                                                                                                                                                                    FILING DATE: 2-Jul-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: ....
STRANDEDNESS: 81...
TOTY: linear
                                                                      STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 ACTITITITICITY
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                                                                                                                                                                                                                                                                       Stephen C. Macevicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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 1.9%;
93.8%;
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Pred. No. 4.
 Score 14.4; DB 1;
Pred. No. 4.3;
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; TOPOLOGY: US-08-283-591-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMURA, JACKIE N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELEPHONE: 415-843-5000
TELEPHONE: 415-843-5000
TELEPAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application of the Patent No. 5629152
GENERAL INFORMATION:
APPLICANT: Ravikums
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                    TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Liberty
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 5629152ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: NOVEL TRISUBSTITUTED TLE OF INVENTION: OLIGO -LACTAMAMIDES MBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                         ENGTH:
                                   TRANDEDNESS:
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15; Conserva
                                                   nucleic acid
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                   linear
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                                 single
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                                                                                                              16:
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US-08-088-658-34/c
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                    Matches
                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25,
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Raviku
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
FILING DATE: N/A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ravikumar, Vasulinga
TITLE OF INVENTION: NOVEL TRISUBSTITUTED
TITLE OF INVENTION: OLIGO -LACTAMAMIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Libert; CITY: Philadelphia STATE: PA
                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5629152ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                   715 CTTTTTTTTTTGATC 730
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                                                                   16 CTTTTTTTTTGGATC 1
                                                                                                                                                  Similarity
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                                                                                                                                   Conservative
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93.8%; Pred. No. 4.3;
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                                                                                                                                   0,
                                                                                                                               Pred. No. 4.3.
0; Mismatches
                                                                                                                                                  Score 14.4; DB 1; Length 16; Pred. No. 4.3;
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Sequence 34, Application US/08088658 Patent No. 5641625

GENERAL INFORMATION:

APPLICANT:

Ecker,

David J.

Buchardt, Ole Egholm, Michael Nielsen, Peter E. Berg, Rolf H.

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2004, 14:10:54; Search time 0.001 Seconds (without alignments) 358.428 Million cell updates/sec

Perfect score: us094770822 753

Sequence:

Scoring table: IDENTITY\_NUC

1 aattagaccgcgtattgaaa...

....tacactggttttttaacctt 753

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

30

15 segs, 238 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Database : 2rni.db:+

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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				SC 1.0 1.0 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4
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170- 175- 132-	-08-088-661F08-150-156A08-108-591B08-087-387-6 -08-461-271-6	75-951-3 75-951-1 83-591-2 83-591-2 83-591-2 88-658-3	-08-461-271-6 -08-713-685A08-713-685A08-471-907A08-477-6 -08-661F08-150A08-150A08-150A-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
sequence 6, Appli sequence 6, Appli sequence 31, Appli sequence 31, Appl sequence 28, Appl	equence 9, equence 1, equence 6, equence 6, equence 6, equence 6	equence 31, equence 16, equence 25, equence 25, equence 34, equence 34,	equence 6, Appequence 6, Appequence 6, Appequence 34, Appequence 6, Appequence 9, Appequence 21,	Description Sequence 6, Appli Sequence 16, Appli Sequence 25, Appli Sequence 25, Appl

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ALIGNMENTS

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US-08-087-387-6
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US-08-455-627-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-087-387-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 358-7855
TELEPHONE: (415) 358-784
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08087387
Patent No. 5473060
                                                                                                                                                                                                                                       Sequence 6, Application US/08455627

Patent No. 5571677

GENERAL INFORMATION:

APPLICANT: Sergei M. Gryaznov

TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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TITLE OF INVENTION: Oligonucle
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,387
FILING DATE: 19930702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 465 Lincoln Centre Drive CITY: Foster City STATE: California COUNTRY. I'c's COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM compatible OPERATING SYSTEM: Windows
                                                                                                                                    ADDRESSEE: Cooley Godward LLP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
                                                                             COUNTRY: USA
ZIP: 94306-2155
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                                                                                                                   California
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31-OCT-2000 (first entry)

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RESULT 10
ADE43355/c
ID ADE43
XX
AC ADE43
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                                                                                                                                                                                                                                                                                              Investigation of silencing of caspase-8 (CASPB) gene by methylation was CC analyzed using methylation-sensitive PCR analysis. Amplification of the CS vuntranslated region (UTR) of the CaspB gene was performed in reaction CC mixtures containing bisulfite treated DNA. Primers AAASIB18-23 were CC designed to produce a 320 bp fragment in the upstream region of CaspB CC gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls CC without DNA were also performed. CASPB, a cysteine protease, is part of CC the death inducing signaling complex (DISC) associated with the Fas CC genomic mathylation FCR analysis of CASPB, a cysteine protease, is part of CC genomic methylation PCR analysis of CASPB gene inactivation. Methylation of the CR can be used to examine even minute amounts of pattient material to CC methods are used to diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASPB in CC gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, colorectal carcinoma, or uterine cervical carcinoma cancer is amplified, such as a neuroblastoma. Aggressive neuroblastoma, colorectal carcinoma, or uterine cervical carcinoma cancer cancer is attended and cancer measured carcinoma. Colorectal carcinoma, or uterine cervical carcinoma compound that induces death-receptor-mediated apoptosis in cells containing an inactivated CASPB gene is also provided
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                                                                                                                                                                                             Query Match
Best Local S
Matches 11
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   ADE43355
                                     ADE43355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 61; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.
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                                                                                                                                                                                                                                                                    Sequence 21 BP; 3 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
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                                       DNA;
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78.6%;
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Pred. No.
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Search completed: March 31, 2004, 14:10:08 Job time: 0.001 secs

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208 19

ACAGGGCTGTGGGGG

222

Query Match Best Local S Matches 11

Similarity

1.1%; 73.3%;

.3%;

Pred Score 8.6; Mismatches

DB 1; 4.

Length 20

Indels

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25-OCT-2001; 2001US-0339525P.
08-NOV-2001; 2001US-0336929P.
08-NOV-2001; 2001US-0338010P.
09-NOV-2001; 2001US-0338363P.
04-DEC-2001; 2001US-0337052P.
28-MAR-2002; 2002US-0368919P.
                           predisposition for or the occurrence of neurodegenerative disease in a subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allalic variant of one or more polymorphic regions of one or more genes selected from upa (Urokinase plasminogen activator), SNCG (gamma-symuclein), IDE (insulindegrading enzyme), KNSLI (Kinesin-like protein 1), LIPA (Iysosomal acid lypase), and TNFSSF6 (Tumour Necrosis Factor Receptor-SF6), where the presence of at least one of the allalic variant of one or more polymorphic regions is indicative of a predisposition for or the occurrence of neurodegenerative disease. The genes are all located on chromosome 10. M1 is useful for determining a predisposition for or the occurrence of, and for treating neurodegenerative disease, particularly Alzheimer's disease. The present sequence is a PCR primer, which was used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6; Alzheimer's disease; neuroprotective; nootropic; gene therapy; Chromosome 10; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human uPA primer, SEQ ID 524.
Sequence 20
                                                                                                                                                                                                                                                                                                                                               Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-559131/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEUR-)
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                                                                                                                                                                                                                                                                The present invention relates to a method (M1) for determining a
                                                                                                                                                                                                                                                                                                 Example
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                                                                                                                                                                                                                                                                                                4; Page 313; 848pp; English.
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Mullin KM,
 BP; 1 A;
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 12 C;
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Sampson AJ,
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5 T; 0 U; 0 Other;
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Blacker [
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RESULT RANGE PROVIDE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor-mediated apoptosis in cells containing an inarrivated C18D8 cama is also warrivated.
The 3' end of this oligonucleotide carries 1,3-propanediol. The cone of four oligonucleotides which were designed to specifically cross-link to the duplex target sequence AAQ20004. Oligo #4 with internal cross-linking group was less effective than the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deoxyribonucleic acid; major groove; ethanoamino group; aziridinylcytosine; cross-linking group; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_base
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                                                                                                                                                                                                                                  New sequence-specific non-photo-activated crosslinking
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                                                                                                                                               Example
                                                                                                                                                                                                   infections e.g.
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                                                                                                                                         2; Page 21; 42pp; English.
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91US-00640654.
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Pred. No. 5.1;
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RESULT 9
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AC AAA6

AAA51823 standard; DNA; 21

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AAA51823;

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                                                                                                                   This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta 'N3'; or (X)m5'-(alpha)n-beta 'N3'; or (X)m5'-(alpha)n-beta 'n nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma; in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                  Peptides PCR.
                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16 BP; 0 A; 2 C; 0 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotides with terminal cross-linking groups.
                                                                                      Sequence 16
                                                                                                           sequences
                                                                                                                                                                                                                                                           Disclosure; Page 10; 19pp;
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                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                AAX18362 standard;
                                                                                                                                                                                                                                                                                                                                                                 Sequence
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14-JAN-1991;
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        Disclosure; Page 10; 19pp; Japanese
                                                                                                       18-JUL-1997;
                                                                                                                        09-FEB-1999.
                                                                                                                                                                          RT-PCR primer; DNA sequence determination;
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91US-00640654.
                                                                    SHUZO CO LTD.
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to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta -N3', or (X)m5'-(gamma)k-delta-N3', where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 13 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X) m5'-(alpha)n-beta
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Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
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Matches Query Match Best Local 15; Similarity Conservative 1.9%; 0 Score 14.4; Pred. No. 3 Mismatches BB ۲, ۳. Length Indels 0 Gaps 0

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            461 TTTTTTTTTTTTTTCA 476
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## 822/c σ

AAA51822 standard; DNA; 21 ВÞ

AAA51822;

31-OCT-2000 (first entry)

Sense primer for untreated CASP8 wild type DNA.

tumour suppressor; death receptor; apo CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; or; chromosome 2q33-34; neuroblastoma; cancer apoptosis; cytostatic; gene therapy; primer; cancer; o o

Homo sapiens

WO200039347-A1

06-JUL-2000

30-DEC-1999; 99WO-US031280

31-DEC-1998; 98US-0114308P

(SJUD-) ST JUDE CHILDREN'S RES

Kidd ٧J, Lahti JM, Teitz <u>,,</u>

WPI; 2000-452423/39

Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.

Example 3; Page 61; 107pp; English.

Investigation of silencing of caspase-8 (CASP8) gene by methylation was analyzed using methylation-sensitive PCR analysis. Amplification of the 5 untranslated region (UTR) of the Casp8 gene was performed in reaction mixtures containing bisulfite treated DNA. Primers AAA51818-23 were designed to produce a 320 bp fragment in the upstream region of Casp8 gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls without DNA were also performed. CASP8, a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the Fas receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation used

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ADE4355
ID ADE35
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ID ADE35
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AC ADE4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Investigation of silencing of caspase-8 (CASPB) gene by methylation was canalyzed using methylation-sensitive PCR analysis. Amplification of the CS unitranslated region (UTR) of the CaspB gene was performed in reaction CC mixtures containing hisulfite treated DNA. Primers AAASIB18-23 were considered to produce a 320 bp fragment in the upstream region of CaspB gene extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls CC without DNA were also performed. CASPB, a cysteine protease, is part of CC the death inducing signaling complex (DISC) associated with the Fas CC receptor. CASPB is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASPB promoter region sequences, in particular CC Region 1 and Region 2, are crucial to the design and execution of the CC gene in a seed to examine even minute amounts of patient material to CC The CASPB gene has been localized to human chromosome 203-34. The CASPB gene has been localized to human chromosome 203-34. The CASPB gene has been localized to human chromosome 203-34. The CASPB gene has been localized to human chromosome 203-34. The CASPB gene has been localized to human chromosome 203-34. The CASPB gene has been localized to human chromosome 203-34. The CASPB gene that expresses a gene enoding functional CASPB in Cells. The cancer that is diagnose or prognose cancer is treated by called the cancer that is diagnosed or treated is a tumour in which a myc gene is amplified, such as a neuroblastoma. Aggressive neuroblastoma, non-small-cell lung carcinoma, con-small-cell lung carcinoma non-small-cell carcinoma non
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                                                                                                                                                                             Neurodegenerative disease; uPA; SNCG; IDE; KNSL1; LIPA; TNFRSF6; Alzheimer's disease; neuroprotective; nootropic; gene therapy; Chromosome 10; PCR; primer; ss.
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RESULT 4
AAQ200G
ID AAQ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method (MI) for determining a CC subject. The method comprises detecting in a target nucleic acid obtained from the subject the presence or absence of an allelic variant of one or more polymorphic regions of one or more genes selected from upa CC (Urokinase plasminogen activator), SNCG (gamma-symuclein), IDE (insulin-CC degrading enzyme), KNSL1 (Kinesin-like protein 1), LIPA (lysosomal acid CC lypase), and THEREFS (Tumour Neorosis Factor Receptor-SF6), where the presence of at least one of the allelic variant of one or more CC polymorphic regions is indicative of a predisposition for or the CC cocurrence of neurodegenerative disease. The genes are all located on CC chromosome 10, MI is useful for determining a predisposition for or the CC cocurrence of, and for treating neurodegenerative disease, particularly C Alzheimer's disease. The present sequence is a PCR primer, which was used in the method of the invention
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Matches 18
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04-DEC-2001;
28-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining a predisposition for or the occurrence of neurodegenerative disease, e.g. Alzheimer's disease by detecting in a target nucleic acid the presence or absence of an allelic variant of one or more polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                    Synthetic.
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                                                                        modified_base
                                                                                                                                                                                                     aziridinylcytosine; cross-linking group;
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Mullin KM,
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100.0%; Pred. No.
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note= "N4N4-ethanocytosine"

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Result
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                                                    CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.
                                                                                                  Sense primer
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Copyright (c) 1993 - 2004 Compugen
                                                                                                   for untreated CASP8
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Investigation of silencing of caspase-8 (CASP8) gene by methylation was call analyzed using methylation-sensitive PCR analysis. Amplification of the Casp8 year was performed in reaction of mixtures containing bisulfitte treated DNA. Primers AAA51818-23 were call designed to produce a 320 bp fragment in the upstream region of Casp8 year extending from nucleotides +221 to +541. Wild type primers were used to amplify the corresponding region of untreated genomic DNA. Controls without DNA were also performed. CASP8 (a speciated with the Fas CC without DNA were also performed. CASP8 (b) a cysteine protease, is part of the death inducing signaling complex (DISC) associated with the Fas CC receptor. CASP8 is inactivated in cancers, and plays a role of a tumour suppressor gene. The CASP8 promoter region sequences, in particular Region 1 and Region 2, are crucial to the design and execution of the genomic methylation PCR analysis of CASP8 gene inactivation. Methylation CC demonstrate whether the CASP8 gene expresses an mRNA and protein product. The CASP8 gene has been localized to human chromosome 2933-34. The call service and the second protein product cells. The cancer that is diagnose or prognose cancer. Cancer is treated by administering a vector that expresses a gene encoding functional CASP8 in call service and service 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting inactivation of a caspase-8 (CASP8) gene for diagnosing or prognosing cancer, comprises detecting a modification of genomic DNA comprising the CASP8 gene that results in inactivation of the gene.
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                                                                                     Juvenile neuroblastoma (preferred), small-cell lung carcinoma, non-small-cell lung carcinoma, colorectal carcinoma, or uterine cervical carcinoma can be diagnosed with the new method. A kit for screening for a compound that induces death-receptor mediated apoptosis in cells containing an
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                                                             inactivated CASP8 gene is also provided
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8 片 Matches Query Match Best Local Sequence 21 90 1 TAGGGGACTCGGAGACTGCGA Similarity TAGGGGACTCGGAGACTGCGA 110 Conservative BP; 5 A; 4 C; 9 G; 3 T; 0 U; 0 Other; 100.0%; 2.8%; 0; Mismatches Score 21; Pred. No. DB 1; 0.52; Length 21; Indels 0 Gaps

0

RESULT 2 AAA51823/c 31-OCT-2000 AAA51823; AAA51823 standard; DNA; 21 BP (first entry)

Antisense primer for untreated CASP8 wild type DNA.

CASP8; caspase-8; promoter; inactivation; methylation; cysteine protease; tumour suppressor; chromosome 2q33-34; neuroblastoma; cancer; death receptor; apoptosis; cytostatic; gene therapy; primer; ss.

WO200039347-A1

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Unclassified.

1 (bases 1 to 16)
1 (bases 2 to 16)
Gryaznov, S.M.
Convergent synthesis of branched and multiply connected macromolecular structures
patent: US 5830658-A 6 03-NOV-1998;
Location/Qualifiers
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AR051238.1
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Gryaznov,S.M. and Lloyd,D.H.
Oligonucleotide clamps having diagnostic applications
Patent: US 5473060-A 6 05-DEC-1995;
Location/Qualifiers
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{\tt Gryaznov}, {\tt S.M.} Convergent synthesis of branched and multiply connected macromomolecular structures
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Sequence 31 from patent US 6451968.
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                                                                                                                                                                                    1 (bases 1 to 15)
Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coull,J.M., Kiely,J. and Griffith,M.
Peptide nucleic acids
Patent: US 6451968-A 31 17-SEP-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent: US 5571677-A 6 05-NOV-1996;
                                                                                                                                                                                                                                                               Unclassified.
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Similarity 90.9%;
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                                                                                                                                                 /mol_type="genomic DNA"
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/mol_type="unassigned DNA"
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                                                                                                                                                              organism="unknown"
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                                                                                                 1.2%; Score 8.8; DI
83.3%; Pred. No. 31;
tive 0; Mismatches
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Pred. No. 27;
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Local Similarity 84.6%;
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149619
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Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and Mollegaard,N.E.
Cleaving double-stranded DNA with peptide nucleic acids
Patent: US 5641625-A 34 24-JUN-1997;
Location/Qualifiers
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                                                   AR371265
Sequence 1 from patent US
AR371265
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Use of nucleic acid analogues in diagnostics and a
                                                                                                                                                                                                                                                                                                                                                                              AR200478
Sequence 21 from patent US
AR200478
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Patent: US 6357163-A 21 19-MAR-2002;
         Unknown
                                          AR371265.1
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Unclassified.
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/mol_type="unassigned DNA"
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                                          GI:34608197
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5641625.
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AR002257/c
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Best Local Similarity 90.9%;
Matches 10; Conservative
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AR002257
AR002257.1
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Buchardt,O., Egholm,M., Nielsen,P.E. and
Peptide nucleic acids
Patent: US 6395474-A 1 28-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 16)
Gryacov, S.M. and Lloyd, D.H.
Oligonuclectide clamps
Patent: US 5741643 A 6 21-APR-1998;
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                                                                                                                                                         1 (bases 1 to 16)
Gryaznov,S.M. and Lloyd,D.H.
Oligonuclectide clamps having diagnostic
                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                        AR045207
Sequence 6 from patent US
AR045207
AR045207.1 GI:5966672
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Similarity 84.6%;
                                                                                                                                               applications
                                                                                                                                                                                                                   Unknown.
                                                                                                                                      Patent: US 5817795-A 6 06-OCT-1998;
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/mol_type="genomic DNA"
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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from patent US 5741643.
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                                                      1.2%;
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0; Mismatches
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Pred. No. 27;
0; Mismatches
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                                           Score 9.4; DB Pred. No. 27; 0; Mismatches
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5817795.
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Morugado, N.A.

Higher-order structure and binding of peptide nucleic acid
Higher-order structure and binding of peptide nucleic acid
Patent JP 199236396-A 8 31-AUG-1999;
ISIS PHARMACEUTICALS INC, BUCHARDT DORUTE, EGUHORUMU MICHAEL, IELSEN
PATER A, BERCH RORUFU HO
OS Unidentified
PN JP 199236396-A/8
PN 1999236396-A/8
PN 1999236396-A/8
PD 31-AUG-1999
PF 14-OCT-1998 JP 1998291590
PF 14-OCT-1998 JP 1998291590
PF 14-OCT-1998 US 088658
PR 02-JUL-1998 US 088658
PR 02-JUL-1993 US 088658
PR 02-JUL-1998 US 1098658
PR 02
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Peptide nucleic acids complexes of two and one nucleic acid strand
Patent: US 5986053-A 34 16-NOV-1999;
Location/Qualifiers
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AR150597
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Double-
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Norden, B., Wittung, P., Buchardt, O., Egholm, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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                                                                                                                                                                                                                                                                                                                 unidentified unidentified
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Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H.,
                                                                                                                                                                                                                                                                                                                                                        E36063.1 GI:13022465
JP 1999236396-A/8.
                                                                                                                                                                                                                                                                                                                                                                                                                  Higher-order structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded peptide nucleic acids Patent: US 6228982-A 9 08-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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/mol_type="unassigned DNA"
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Pred. No. 2
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de nucleic acid.
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640 CCCAAAAAACAAG 652
1.3%;
il Similarity 84.6%;
11; Conservative
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142187
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Ravikumar,V.

Trisubstituted .beta.-lactams and oligo .beta.-lactamamides

Patent: US 5629152-A 16 13-MAY-1997;

Location/Qualifiers
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Sequence 16 from patent US 5629152.
I42181 I32181.1 GI:2467676
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                                                                                   Trisubstituted .beta.-lactams and oligo Patent: US 5629152-A 25 13-MAY-1997; Location/Qualifiers
                                                                                                                          1 (bases 1 to 16)
Ravikumar, V.
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C12N15/09,C12Q1/68,C12N15/00
Strandedness: Single;
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="unassigned
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                                                 'mol_type="unassigned DNA"
                                                              organism="unknown"
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   0; Mismatches
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RESULT 15
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Buchardt,O., Egholm,M., Nielsen,P.E. and
Peptide nucleic acids
Patent: US 6395474-A 1 28-MAY-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Sequence 1 from patent US
AR371265
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Patent: US 6357163-A 21 19-MAR-2002;
Location/Qualifiers
 AR231294 . 1
Sequence 31 from patent US
AR231294
AR231294.1 GI:27272225
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Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
Use of nucleic acid analogues in diagnostics and a
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Sequence 21 from patent US
AR200478
                                                                                                                                                                                                                                                                                          Unknown
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                                                                                                                                         h 1.9%; Score 14.4; DB 1;
Similarity 93.8%; Pred. No. 4.3;
15; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                               Unclassified.
                                                                                                                                                                                                                                                                                                      Unknown.
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larity 93.8%; Pred. No. 4.3;
Conservative 0; Mismatches 1;
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/mol_type="genomic DNA"
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Matches 14
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TITLE
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Best Local Similarity 84.6%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                         source
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WSE OF NUCLEIC ACID ANALOGUES IN THE INI

AMPLIPICATION

Patent: WO 9325706-A 3 23-DEC-1993;

BUCHARDT OLE (DX)

Other publication CZ 9402951 950913

Other publication AU 4323593 940104

Other publication AU 4323593 940104

Other publication SX 121683 1931223

Other publication SX 149394 960110

Other publication HU 71931 960228

Other publication WO 944655 950203

Other publication WO 944655 950203

Other publication JP 8501681T 960227.

Location/Qualifiers
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Sequence
AR087164
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Egholm, M., Nielsen, P., Buchardt, O., 1

Coull, J.M., Xiely, J. and Griffith, M.

Peptide nucleic acids 17-SEP-2002;

Patent: US 6451968-A 31 17-SEP-2002;

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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/mol_type="genomic
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from patent US 5986053.
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1 (bases 1 to 16)

1 (bases 1 to 16)

1 (pases 1 to 16)

2 (pases 1 to 16)
                                                                                                                                                                                                                                                                                                                                          Gryaznov,S.M.

Convergent synthesis of branched and multiply connected macromomolecular structures

Patent: US 5571677-A 6 05-NOV-1996;

Pocation/Qualifiers
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Sequence 6 from patent US 5571677.
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/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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/mol_type="unassigned DNA"
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142181
142181.1 GI:2467676
                                                                                                                                                Sequence 34 from patent US 5641625. 149619 149619.1 GI:2471839
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Ravikumar, V.
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Location/Qualifiers
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                              Cleaving double-stranded DNA with peptide nucleic acids Patent: US 5641625-A 34 24-JUN-1997; Location/Qualifiers
                                                                  1 (bases 1 to 16)
Ecker, D.J., Buchardt, O., Egholm, M., Nielsen, P.E., Berg, R.H. and Mollegaard, N.E.
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Ravikumar, V.
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           organism="unknown"
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_type="unassigned DNA"
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Local Similarity 93.8%;
                                                                                                                                                                                                                                                                          459
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                                                                                                                                                      Sequence 34
AR087164
AR087164.1
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                                                                   1 (bases 1 to 16)
Ecker, D.J., Buchardt, O.,
Mollegaard, N.E.
                                                                                                                                                                                                                                                                                                                                                                               Convergent synthesis of branched and macromolecular structures
Patent: US 5830558-A 6 03-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 16)
Gryaznov, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6 from patent AR051238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases I to 16)
Gryagnov,S.M. and Lloyd,D.H.
Oligonucleotide clamps having diagnostic and therapeutic
                                   Peptide nucleic acids complexes of two peptide nucleic acid and one nucleic acid strand Patent: US 5986053-A 34 16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent: US 5817795-A 6 06-OCT-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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                                                                                                                                                                          16 bp
34 from patent US 5986053.
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            /organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
/organism="unknown"
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O; Mismatches
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                                                                                Egholm, M., Nielsen, P.E.,
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                                                                              Berg, R.H.
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AR150597/c
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Best Local Similarity 93.8%; Pred. No. 4.3;
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Sequence 9 :
AR150597
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Higher-order structure and binding of peptide nucleic acid.
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Patent: US 6228982-A 9 08-MAY-2001;
Location/Qualifiers
1. .16
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Bushato,O., Eguhorumu,M., Nielsen,P.A., Berg,R.H.,
Morugado,N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          Higher-order structure and binding of peptide nucleic acid Patent: JF 1999236396-A 8 31-AUG-1999; ISIS PHARMACEUTICALS INC, BUCHARDT DORUTE, EGUHORUMU MICHAEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E36063.1 GI:13022
JP 1999236396-A/8.
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Norden, B., Wittung, P., Buchardt, O.,
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/ \verb| organism=' Unidentified'|.\\ Location/Qualifiers
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/mol_type="unassigned
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Maximum Match 100%
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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14.4
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(without alignments)
359.934 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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 BB
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AR002257
AR045207
AR051238
AR087164
AR150597
E36063
I18032
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I42181
A36563
AR087164
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AR051238
118367
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AR200478
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         ACCESSION: A36563
ACCESSION: AR062257
ACCESSION: AR051238
ACCESSION: AR051238
ACCESSION: AR3663
ACCESSION: 1283663
ACCESSION: 128367
ACCESSION: 142181
ACCESSION: 142181
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ACCESSION: AR371265
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ACCESSION: A36663
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ALIGNMENTS

RESULT 3 AR045207 ACCUS ADEFINITION SA	Qy 459 Db 1	Query Match Best Local : Matches 1:	L F SE SW	RESULT 2 AR002257 LOCUS DEFINITION SACCESSION AND VERSION AND VERSION AND XEYWORDS	Qy 715 Db 16	Query Match Best Local S Matches 15	FEATURES SOURCE	JOURNAL PE  COMMENT OF	REFERENCE 1 AUTHORS Buc TITLE USE AMP	×S	RESULT 1 A36563/C A36CUS A3ACCESSION A3VERSION A3ACCESSION A3ACCES
AR045207 Sequence 6 from patent US 5817795.	ACTITITITICITITI 474	1.9%; Score 14.4; DB 1; Smilarity 93.8%; Pred. No. 4.3; Similarity 93.8%; Pred. No. 4.3; Similarity 0; Mismatches 1;	Unknown. Unclassified. 1 (bases 1 to 16) 1 (base	AR002257 16 bp DNA Sequence 6 from patent US 5741643. AR002257 AR002257.1 GI:3963811	CTTTTTTTTTGATC 730	1.9%; Score 14.4; DB 1; imilarity 93.8%; Pred. No. 4.3; ; Conservative 0; Mismatches 1;	other publication SK 149394 960110 other publication HU 71931 960228 other publication FI 945725 941205 other publication WO 944655 950203 other publication JP 8501681T 960227. Location/Qualifiers 1. Coation/Qualifiers 1/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon;32644"	:: WO 9325706-A 3 23- publication CZ 94029 publication AU 43235 publication CA 21368	i (bases 1 to 16) Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. USE OF NUCLEIC ACID ANALOGUES IN THE INHIBITION AMPLIFICATION	unidentified unidentified unidentified unolassified.	A36563 Sequence 3 from Patent W09325706. A36563 A36563.1 GI:2293876
linear		Length 16; Indels		linear		Length 16; Indels		-	and OF		linear
PAT		0,		PAT		0			Star		PAT
29-SEP-1		Gaps		04-DEC-1		Gaps			Stanley, C.J.		05-MAR-1997
1999		0;		8661		0,			•		.997

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The present invention relates to methods and oligonucleotides for forming CC a triple-helix comprising a double helical nucleic acid comprising first CC and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel CC orientation, respectively, to target sequences on alternate strands of the double helical nucleic acid. The method has therapeutic applications, where gene expression is controlled by selective triple-helix formation CC where gene expression regulatory sequences of a target gene. The coligonucleotides can be used to form triple-helices, and are useful to detect the presence or absence of specific sequences within genomic DNA CC for diagnostic and therapeutic purposes. The oligonucleotides can be used to form triple-helices, and are useful to secific sequences required by pathogenic double-stranded DNA including specific sequences required by pathogenic double-stranded DNA including the oligonucleotide can be chosen to target a unique sequence of the CC suppression or virulence, reducing their pathogenicity. Alternatively, CC suppression of specific onogenes including those of endogenous or viral corigin. Such therapeutic oligonucleotides are capable of forming triple-helix corigin. Such therapeutic oligonucleotides are capable of forming triple-helices with such sequences in cancerous cells containing the activated concogene, so preferentially killing or repressing the cancer causing cell. The present sequence represents an ollgonucleotide used in the methods of the present invention
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Search completed: March 31, 2004, 14:06:04 Job time: 0.001 secs В Query Match 1.2%; Best Local Similarity 76.9%; Matches 10; Conservative 255 AGGCAAAGGGAAA 267 15 AGAGAAAGAGAAA 3 <u>,</u> Score 8.2; Pred. No. 0; Mismatches DB 1; Length 15; 3; Indels 0 Gaps

0

Sequence 15 BP; 0 A; 4 C; 0 G; 11 T; 0 U; 0 Other;

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RESULT 3
AAH20313/c
ID AAH20313;
XX
AC AAH20313;
XC AAH20313;
XC AAH20313;
XC DNA-EDTA-FE(II) probe 7.
XX
DE DNA-EDTA-FE(II) probe; DNA cleavag
XX
COS Synthetic.
XX
FM Key
FT modified_base /*tag= b
FT /mod_base= OTHER
FT /mod_
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonuclectide which binds in parallel and antiparallel orientation, respectively, for targetting sequences on alternate strands of DHNA to control gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods and oligonucleotides for forming a triple-helix comprising a double helical nucleic acid comprising first and second substantially complementary strands, and an oligonucleotide bound to a purine-rich target sequence within the double helical nucleic acid, where the oligonucleotide binds in a parallel and antiparallel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridisation probe; DNA cleavage; double-helix; oncogene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%;
Conservative
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/note= "Thymidine has
C-5"
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RESULT 4
ABK9811
XX
ABK9811
XX
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O7-OCT
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Tripl
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Matches 10
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12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triple-helix formation; purine-rich target sequence; double-helix Dygene expression; regulatory sequence; pathogenic double-stranded DN pathogenic bacteria; virus; replication; virulence; cancer; oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15
                                                                                                                                                                                                                                                       17-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                     11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triple helix forming associated oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK98147 standard;
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                                                                                                                                                                                                                                                                                                                16-DEC-1993;
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93US-00152250.
                                                                                                                                                                                                                                                       92US-00946976
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Pred. No. 0;
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A triple-helix comprising a double helical nucleic acid (DHNA) and an oligonucleotide which binds in parallel and antiparallel orientation,

WPI; 2002-536030/57.

(CALY ) CALIFORNIA INST

OF TECHNOLOGY

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RESULT 1
AAH20313
ID AAH2
XX AAH2
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AC AAH2
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XX JAH2
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Perfect score:
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Listing first 20 summaries
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      31-MAY-2001.
                                                             US2001002314-A1.
                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                               Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-EDTA-FE(II)
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                                                                                                                                               "Thymidine has EDTA-FE(II) covalently attached
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DNA-EDTA-FE(II) pr
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Matches
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16-NOV-1990;
12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. BDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-helical DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention which is used in an example illustrating how it binds to and cleaves a double stranded fragment of
                                                                                                                                                         US6403302-B1
                                                                                                                                                                                                                              Triple-helix formation; purine-rich target sequence; double-helix gene expression; regulatory sequence; pathogenic double-stranded pathogenic bacteria; virus; replication; virulence; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.
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                                                                      17-SEP-1992;
                                                                                                                             11-JUN-2002
                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                     Triple helix forming associated oligonucleotide #30
                                                                                                                                                                                                                                                                                                                    07-OCT-2002
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                                       (CALY ) CALIFORNIA INST OF TECHNOLOGY
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Initial Score = Residue Identity =
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                                                                                                                                                                                                                                                                                                                              31. US-09-477-082-2 (1-753)
US-09-477-082-22 Sequence 22, Application US/09477082
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US-09-477-082-18 Sequence 18, Application US/09477082
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US-09-477-082-34 Sequence 34, Application US/09477082
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57% Matches = 12
0 Conservative Substitutions
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43% Matches = 10
0 Conservative Substitutions
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52% Matches = 11
0 Conservative Substitutions
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Matches = 13
Conservative Substitutions
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12 Mismatches = 9
ions = 0
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13 Mismatches = 12
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X 10 20
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32. US-09-477-082-2 (1-753) US-09-477-082-30 Sequence 30, Application US/09477082

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Initial Score = 5 Optimized Score = 11 Significance = -0.27
Residue Identity = 50% Matches = 11
Gaps = 0 Conservative Substitutions = 0
AATTAGACGCGTATTGAAAGTAAAGAACTTCTTCCTGGGAAGCCTTTCCCACCCCCTTCCCTGGCAAGCA
X 10 20 X
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80 CGTGGAGT

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Initial Score =
Residue Identity =
Gaps =
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US-09-477-082-21 Sequence 21, Application US/09477082
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US-09-477-082-25 Sequence 25, Application US/09477082
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US-09-477-082-28 Sequence 28, Application US/09477082
                                                                                                                                                                                                                                                                          23. US-09-477-082-2 (1-753)
US-09-477-082-15 Sequence 15, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X 520 530 540 550 560 TGTCATTGTCGAATGCCCTGAGGTGCACAGCCCCTTTCCCCT
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CCCTGCCCTCTGTTTTTGTTGCCCAAAAAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTA
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CTTGGATCTGCCCTTCTGAGGACACCTCTGGTGCTGCCTGGCCCAGGTCT
                                                                                                                           170 180 190 200 210 X 220 230 X TTCAACAGGAAACAGGGCTGTGGGGGAAGGAA
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54% Matches = 12
0 Conservative Substitutions
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Matches = 10 Mismatches = 10
Conservative Substitutions = 0
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Matches = 14
Conservative Substitutions
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14 Mismatches = 9
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12 Mismatches = 10
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X 10 20
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X 10 20 X
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Initial Score = Residue Identity =
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Residue Identity =
Gaps =
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US-09-477-082-16 Sequence 16, Application US/09477082
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US-09-477-082-20 Sequence 20, Application US/09477082
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US-09-477-082-23 Sequence 23, Application US/09477082
                                                                                                                                                                                                  Initial Score = 8 Optimized Score = 14
Residue Identity = 66% Matches = 14
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                         27. US-09-477-082-2 (1-753)
US-09-477-082-17 Sequence 17, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 290 250 X
TTCTTGACTTGCTCTAGAAACAGGGCTGTGGGGGTGGGGGAAGCAACTTGGATCTGCCCTTTTTGAGACACCT
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130 140 150 160 170 GTGGAGCGGGTGAGAGCGGAAAC
                                                                                                                              60 70 80 100 X 110 120 X CCCCCTTCCCTGAGCACGTGGAGTTAGGCAGGTAAGGTTAGGGGAACTTCGGAGGACTTCCGATGGTGCCAGGAAAGG
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52% Matches = 11
0 Conservative Substitutions
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42% Matches = 9
0 Conservative Substitutions
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11 Mismatches = 10
ions = 0
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14 Mismatches = 7
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9 Mismatches = 12
ons = 0
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9 Mismatches = 11
ons = 0
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                                                                      GATGACATGGTGCCTGGGAAC
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X 10 20
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28. US-09-477-082-2 (1-753) US-09-477-082-32 Sequence 32, Application US/09477082

TTTGTTTCTTGACTTGCTCTAGAAACAGGGCTGTGGGGGGTGGGGAAGCAA

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Initial Score = Residue Identity = Gaps =
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Residue Identity = 80% Matches = 16
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14. US-09-477-082-2 (1-753)
    US-09-477-082-31 Sequence 31, Application US/09477082
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US-09-477-082-13 Sequence 13, Application US/09477082
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650 660 670 680 700 710 720
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US-09-477-082-19 Sequence 19, Application US/09477082
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TGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTGTTTCTTC
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80% Matches = 17
0 Conservative Substitutions
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Matches = 14
Conservative Substitutions
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17 Mismatches = 4
tions = 0
                                                                                                                                       14 Significance = -0.21
14 Mismatches = 8
ions = 0
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16 Mismatches = 4
ions = 0
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X 10 20
                                TTCAGCAAAGTACCGCAATTTC
X 10 20 X
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Initial Score = Residue Identity = Gaps
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US-09-477-082-27 Sequence 27, Application US/09477082
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US-09-477-082-14 Sequence 14, Application US/09477082
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US-09-477-082-24 Sequence 24, Application US/09477082
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    US-09-477-082-26 Sequence 26, Application US/09477082
100 110 120 130 140 150 GGAGACTGCGATGCCAGGAAAAGGGTGGAGTGAGTGCCTGTTGCC
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CGTGGAGTTAGGC
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11 Mismatches = 11
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15 Mismatches = .9
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Mismatches = 10
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Initial Score = Residue Identity = Gaps = Figure 1
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US-09-477-082-6 Sequence 6, Application US/09477082
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US-09-477-082-33 Sequence 33, Application US/09477082
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520 530 540 550 560 570 580
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TCTCTAAACGTTTTCGATGTGGA-----TFCGCGGAAATTAACCTGCACTCGCAAAATGAACTTTT
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Matches = 86
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US-09-477-082-8 Sequence 8, Application US/09477082
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US-09-477-082-29 Sequence 29, Application US/09477082
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AGAAAATCCTTCTTATGCCTATTTTTTTTAAATCAAAAGGGATTTAACATAGCTATACCAAAAGGGCCATG
440 450 460 470 480 490 500
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150 160 170 180 190 200 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $06
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33% Matches = 252 Mismatches = 501
9 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = 19
Matches = 19
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 Significance = -0.16
19 Mismatches = 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGGGGATTCGGAGATTGCGA
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X 10 20
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Initial Score =
Residue Identity =
                                                                                                                                                                                                                                 Initial Score = Residue Identity = =
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US-09-477-082-5 Sequence 5, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                          7. US-09-477-082-2 (1-753)
US-09-477-082-10 Sequence 10, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 470 480 490 500 500 Aprovantorarization of the second 
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170 180 190 200 210 220 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 320 330 340 350 360 370 ATGCCTTTGACTCTGAGCAGTCTCCAGTTCCTGCTACCTTTTTTGTCCTCCAAGC
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100 110 120 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAACCTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-TACAACCTGCAGATATTTTCATAGAGATGGAGAAGAGGGTCATCCTGGGAGAAGGAAAGTTGGACATCC
240 250 260 270 280 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCGCAATTTCCTATGTTTTAACGCAGCATAGGTCAGAAGGGGGGCCTGCGCAGCTCGATAATCT
390 X 400 410 420 430 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAAAGAGTCTGTGCCCAAATCAACAAGAGCTGCTGAAGATAATCAACGACTATGAAGAATTCAGCAAAG
0 320 330 340 350 360 370 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTTTTTTAACCTT
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32% Matches = 131
2 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                690
                                                                                                                                                                                                                                                                               Optimized Score = Matches =
                                                                                                                                                                                                                                 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710
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Mismatches = 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGACTGGGTGACATCTGACA
                                                                                                                                                                                                                                           Significance = -0.08
Mismatches = 134

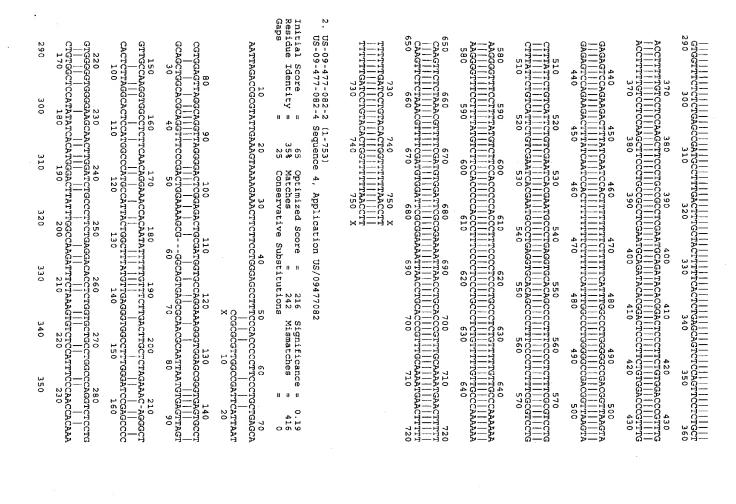
0
CTTCGTGGTCTGTCTCTGGGCC
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Initial Score = Residue Identity = Gaps =
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US-09-477-082-9 Sequence 9, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGATGCCTCAGCCTACTTTCACACTAAGAAAAAACTTGTCTTTCCCCTTCTGATTGA
. 170 180 190 200 210 220 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 520 540 550 550 STORY THE STORY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cochedececederretecerectececeteaetecetedearaeterereaataetreeaataeceari
30 40 50 60 70 80 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTATGÁ-CÁTTTTGAÁAAATCTACCAACTCATGGÁCCACAGTAACATGGACTGCTTCATCTGCTGATCTCT
170 180 190 200 210 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGCGTATTGAAAGTAAAAGAAACTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCACGTGGA
                                                                                                                                                                                                                                                                                              CTCAGTTCACTGTTTGAAGTGCCCTTCCCTTGCTGAAAAACCCAAAGTGTTTTTTATTCAGGATTGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              370 380 390 400 410 420 420 TTTGTCCTCCAACCCTTCTGTGGACCCGTTTGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCCATGCAGCACAACGCCATCATCTATGCCACTGATGGAC----AGGAGCCCCCCCATCTATGAGCTGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGÓGCTTTGAĆCAĆGÁCTTTGÁÁGAGCTTCÁTTTTGAGATCAAGCCCCAĆGATGACTGCÁCAGTAGAGCAA
100 110 120 130 140 150 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCTGCACTCTCCCTGCTGCTGCTGCTGCTATAGTGTGGCGTACTGTTCGAGTTTCACT-TTTC
                                                                                                                                               440
TCCAGAAGACTTTATCAATCCACTTTTTTTTTTTTCATTTGCCCCTGGGGGCGACGGTTAAGTACTTTA
--GGĠĀTAĀĊŢĀCCAGĀĀĀGGTĀŢĀCCTGTŢGĀGAGAĞTĞĀTŢCĀĠĀGGĀGCĀACCCTĀTTTĀGĀĀĀTGGĀTĨT
380 390 400 410 420 430
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36%
06
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Matches = 260
Conservative Substitutions
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Mismatches = 429
s
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X 10 20
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Initial Score = Residue Identity = Gaps =
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US-09-477-082-3 Sequence 3, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 490 500
GGAGAGTCCAGAAGACTTTATCACTTTTTTTTTTTTTTGGCCCTGGGGGCCGACGGTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGCAAGAAGAATGGCATATTACTTGCCGCCGACGAGGGTTATTATTACTAAATGGAGTCAGTATAAATGC 290 300 310 320 330 340 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CÁTGGGGGTTAAATÁAAGCGCTTT
650 660 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710 650 X AACAAGTTCTCTAPACGTTTTCGATGTGGATTCGCGGAAAATTAACCTGCACCCGTTTGCAAAATGAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCCAATAAAGCATGTCCAGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTC
60 370 380 390 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 60 70 80 90 100 110
GCCTTTCCCACCCCTTCCCTGCTGAGCACGTGGAGTTAGGCAGGTTAGGGGACTCGGAGACTGCGATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCGCGCCCAGCCCATTGGCTTGTTTTGTÅTGTCTAĆCTTCCTAAACAGTAÁGAGGGAACTTGTCTGGTGT
230 240 250 260 270 280 290 GAAGCAACTTGGATCTTGGATCTTGGATCTTGGATCTTCTCTGATGGATCTTGGATGTTTCTC
                                                                                                                                            TTAAAAAGATGGACTTCAGGAGAAATCTTTATGATATTGGGGGAAAACTGGAACAGTGAAGATCTGGGCCTCCCC 220 230 240 250 260 270 280
                                                                                                                                                                                                                                                                          120 130 140 150 150 160 150 CCAAGGAAAGGGT------GGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTTTTTCTCTCCTGTGCTGACAGGACAATGACCAGTACCTAGTAGTTGCAGTAGCCTTTGATGAACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 236
Matches = 305
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X 10 20 30 40 Aprilagacçocorarios Aprilagacçocorarios Aprilagacçocorarios Aprilagacçocorarios Aprilagacços Ap
                                                    260
                                                    270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 Significance = -0.04
305 Mismatches = 448
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Initial Score = Residue Identity = US-09-477-082-2 (1-753)
US-09-477-082-7 Sequence 7, Application US/09477082 gcadagadteááartrotacótácaganagatagaaactccartatádaactidadaáatatagadattaaarag 510 520 530 540 550 550 AGAĞACYCCAĞAAAAGAĞAATGTTGGĞGGAAAGCAATCTGTCCTTCCTGAAĞGAGCTGCTCTTCCGAATTA
370 380 390 400 410 420 430 TCAAGTTCCTGAACTGAACTACATTCCGCAAAGGAAGCAAGAACCCATCAAGGATGCCTTGATGTTATTCC АТАРАНТАРАЛІТТ Х 870 GAAGÁTGTCCCÁCCGGAGCCAGAÍTAAGÁÁÍTTTÁGGGGGCCTTATAÍTATAATTCTATÁGAAAÍGCTAAGÁCC 800 810 820 830 840 850 ATAGAĊTGĠĀŤŤTGĊŤĠATTACĊTĀĊCTĀAĀĊĀCTAGAĀĀĠĠĀGGAGĀŤGGAĀĀĠĠĢAĀĊTŤCĀĠĀCACCĀĠ 440 450 460 470 480 490 ATTĊTAAAGĊTTĊTACAGAAGACAGTAGTGCCCTTGGTGGTCCTGCTAAAGGCTGTAAAACCTTAGCTTCTCCCC 50 660 670 680 690 700 710 720 TTCCCGGGTTTTCCCGAGGGGGAGGAGTTGTGTGGGGTAATGACAATCTCGGACTCTCCAAGAGAGAACACGAT 39\* 39\* Optimized Score = Matches = Conservative Substitutions 60 64 Significance = -0.07 69 Mismatches = 102 580 CGGGTCACCCTTGGGGTAAATT X 10 20

690



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Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 370 380 390 400 410 410 420 430 TACCITTTIGECTCAAGCTECCTGCCCCCCGAATGCAATACACGGACTCCCTTCTGGGACCCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-477-082-2 (1-753)
US-09-477-082-1 Sequence 1, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                ÁAGCGCTCCAAGACACGÁTTGCÁGÁAGGÁAC-ACGGGGTCGAACTGAAATTTGAAGAACAGGÁCCAÁGGÁ
X 10 20 30 40 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÁGÁCCAÍDAAATÁÁAAAÍTÍ--ÁÍTTTTCAAAGTGAÁÁCATÍACTTAGAGGTATGCTGAAGTTATÁÁTAGAG
180 590 600 610 620 630 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOTGOTTTTCTCTCAGCCGATGCCTTTGACTTTGCTACTTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGC
GAGAGGGCTGGTCTGTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAGGGAAACTTCCTATTCCCAGACCCT 220 230 240 250 260 270
                                                     TCCTTTTTTTCTGAACGATCTACCCÁTTTCA GCCÁCAGGCTGACTTTACCCAGTCCGGCGGGGGGAG
150 160 170 180 190 200 210
                                                                                                                                                                      TGGGAACTCAGCCTGAGCACGGGTTGATCCGGAGCAGCGGCTTACCGAACTACGAACTAGAACCAGACCACTTCC 80 100 100 110 120 130 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTTGATCCTGTACACTGGTTTTTTTAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGGGAAGATGTCCCACCGGAGCCAGATTAAAATTTAAGAGGGCCTTATATAATTCTATAGAAATGCTA
510 520 530 540 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACAATTCTAAGCTTCTACAGAAAAAGACAGTAGTGCCTTGGGTGGCCTGCTAAAAGGCTGTAAAACTTAGCT
370 380 390 400 410 420 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTAAGTTTCTTTTGCAAGAGGAAATCTCCAAATGCAAACTGGATGATGACATGGTGCCTGGGAACAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 Optimized Score = 219
36% Matches = 243
5 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ATTTCAGAAGAAGÍĠĀĠĊĀĠĀTCAGĀĀŤTGAGGĪCT
260 270 280 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 Significance = -0.03
243 Mismatches = 424
utions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340
```

## 09477082-2vs09477082-\_.res 1d 2 VS. Ž to help locate primers

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US-09-477-082-2 Sequence 2, Application US

753

753

753

5.45

3 8

Page

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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                       STORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 v <u>o</u> v
o o v
                                                                                                  Number of
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Number of
                                                                                                                                                                                                                                                                                                                                                                      SHUZHCOHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AO MEBRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query sequence being compared:US-09-477-082-2 (1-753) Number of sequences searched: 32 Number of scores above cutoff: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Results file 09477082-2vs09477082-_.res made by spaul on Wed 31 Mar 104 14:27:27-PST.
Sequence Name
                                                        The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                      Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                        Times:
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                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results of the initial comparison of US-09-477-082-2 (1-753) with: File : US09477082.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IntelliGenetics
                                      identical
                                                                                                  residues:
sequences searched:
scores above cutoff:
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48
—
                                     sequence to the
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     Description
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00:00:00.00
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2
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                                                                                                                                                                                                                                                                                                        PARAMETERS
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5
                                     query sequence was found:
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Joining penalty
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                                                                                                                                                                            Standard Deviation 130.74
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1. US-09-477-082-2 (1-753) US-09-477-082-2 Sequence 2, Application US/09477082 Optimized Score = 753 Matches = 753 Conservative Substitutions Significance = Mismatches =

5.45

100%

Initial Score = Residue Identity = Gaps = = AATTAGACCGCGTATTGAAAAGTAAAAGTTCTTCCTGGGAGCCTTTCCCACCCCCTTCCCTGCTGAGCA X 10 20 30 40 50 60 70 AATTAGACCGCGTATTGAAAGTAAAAGAACTTCTTCCTGGGAGCCTTTCCCACCCCCCTTCCCTGCTGAGCA 20

GTTGCCAAGGTGGCCTCTTCAACAGGAAACCACAATATTTTTGTTTCTTGACTTGCTCTAGAAACAGGGCTG 

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Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score = Residue Identity = Gaps =
                                                                                                                                         Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24. US-09-477-082-1 (1-670)
US-09-477-082-27 Sequence 27, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23. US-09-477-082-1 (1-670)
US-09-477-082-17 Sequence 17, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22. US-09-477-082-1 (1-670)
US-09-477-082-29 Sequence 29, Application US/09477082
                                                                                                                                                                                                          25. US-09-477-082-1 (1-670)
US-09-477-082-25 Sequence 25, Application US/09477082
                                                                                                                                                                                                                                                                                                                                      560 570 580 590 600 610 CTCTCTCGGAGACCCAGATTCTCACAGG
                                                                                                                                                                                                                                                                                     ×G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 20 30 40 50 \rm X 60 \rm 70 \rm X CGCTCCAAGACACGATTGCAGAACAGGACCGAACGATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           490 500 510 520 530 540 550 AGTGAGTCATCTTCTGTGTGTGAGTGTTTCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 90 100 110 120 ACTCAGCCTGAGCACGGTTGATCCGAGCAGGAGCAAGTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    580 590 600 610 620 CTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGGTTCTCCTTCTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCTTTTCTCTCGGAGACCAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 290 300 310 CTATTCCCAGACCCTTTGCCAGAAGAAAGGAATGGCATATTACTTGCCGCCG
                                                                                  220
 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42%
0
                                                                                                                                          50%
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 Optimized Score = 12
50% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 Optimized Score = 8
38% Matches = 8
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Optimized Score = 9
Matches = 9
Conservative Substitutions
                                                                                                                                       Optimized Score = 10
Matches = 10
Conservative Substitutions
 240
250
260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 Significance = -0.23
12 Mismatches = 12
                                                                                                                                         10 Significance = -0.24
10 Mismatches = 10
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 Significance = -0.23
8 Mismatches = 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGGGGATTCGGAGATTGCGA
                               GÁTGCÁGGTGGGGGGGCTC
X 10
                                                                                                                                                                                                                                                                                                                                                                                           TGTCCTCGGTAAGTTTTGCCTA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGACATGGTGCCTGGGAAC
X 10 20
```

Initial Score = Residue Identity = Gaps =

TATTTTGÁCTTAGATTÁTATTC X 10 20 Optimized Score = 8 Significance = -0.24 Matches = 8 Mismatches = 15 Conservative Substitutions = 0

```
Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                              Initial Score = Residue Identity = Gaps =
29. US-09-477-082-1 (1-670)
US-09-477-082-14 Sequence 14, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                       28. US-09-477-082-1 (1-670)
US-09-477-082-21 Sequence 21, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27. US-09-477-082-1 (1-670)
US-09-477-082-30 Sequence 30, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26. US-09-477-082-1 (1-670)
US-09-477-082-34 Sequence 34, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 430 440 450 450 CCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAAC
                                                                                                                                                                                                                                                    350 x 400 410 GTCAGTATAAAGCATGTCCAGCGCCTCGGGCTTTAGTTTGGACGTCCATGAATTGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 510 520 530 540 CTCTGTTCTGTTTAGGAGTAAAGTTTACCCTGCAGTTCCTTCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGGGCTGGTCTGACTTCAGTGCTGAGGTTTGATCAAGGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 Optimized Score = 10
45% Matches = 10
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 Optimized Score = 8
38% Matches = 8
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                              6 Optimized Score = 11
47% Matches = 11
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                11 Significance = -0.24
11 Mismatches = 12
utions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 Significance = -0.24
8 Mismatches = 13
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 Significance = -0.24
10 Mismatches = 12
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTATATCTACATTCGAAACGA
X 10
                                                                                                                                                                                                   TCAAATGTTAGTTAATTTACTA
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGTATCTGCATTCGAGGCG
X 10 20
```

```
Initial Score = Residue Identity =
                                                                                                                                                             17. US-09-477-082-1 (1-670)
US-09-477-082-23 Sequence 23, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial Score = 9
Residue Identity = 47%
Gaps = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score = 9 Optimized Score = 13
Residue Identity = 59% Matches = 13
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initial Score = 9 Optimized Score = 10
Residue Identity = 47% Matches = 10
Gaps = 0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16. US-09-477-082-1 (1-670)
    US-09-477-082-26 Sequence 26, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15. US-09-477-082-1 (1-670)
US-09-477-082-19 Sequence 19, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14. US-09-477-082-1 (1-670)
US-09-477-082-33 Sequence 33, Application US/09477082
560 570 580 590 600 X 610 620 X CTCTTTCTCTCGGAGACCAGATTCTGCCTTTTACCTGGAGGGAAGTGTTTTCACAGGGTTCTCCTCCTTTTAT
                                                                                                                                                                                                                                                                  ×a
                                                                                                                                                                                                                                                                                                                           X 570 580 590 600 610 CGGAGACCAGATTCTGCCTTTACGCTGGAGGGAAGTGTTTTCACAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                             110 120 130 140 150 X 160 170 X AGCAGGGCTAAGCCAAGTACGAATCAACCAGACCACTTCCTCCTTTTTTTCTGAACGATCTACCGCATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 590 600 610 620 CTGCCTTTACGCTGGGGAAGTGTTTTCACAGGTTCTCCTCCTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 650 660 670 GTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 520 530 540 550 X 560 570 X TGCTTTAGGAGTTTACCCTGCAGAGACAGATTCTCTGTGAAGATTTCTCTTTTTTCTCTGGAGAGACCAGATT
                                                                                  8 Optimized Score = 9 Significance = -0.22
42% Matches = 9 Mismatches = 12
0 Conservative Substitutions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Optimized Score = 11
Matches = 11
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 Significance = -0.21
10 Mismatches = 11
1tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 Significance = -0.21
13 Mismatches = 9
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 Significance = -0.21
11 Mismatches = 12
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCCTCCTCTTACAACCTG
                                                                                                                                                                                                                                                                                                                                                                                           AGTÍTCÁCTÍTÍTCAGGGGCÍTTÍ
X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGGGGACTCGGAGACTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCAGCAAAGTACCGCAATTT
```

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Initial Score = Residue Identity = Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Score = Residue Identity = Gaps =
                                                                      Initial Score = Residue Identity = Care
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Initial Score =
Residue Identity =
Gaps =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19. US-09-477-082-1 (1-670)
US-09-477-082-15 Sequence 15, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18. US-09-477-082-1 (1-670)
US-09-477-082-24 Sequence 24, Application US/09477082
                                                                                                                                   21. US-09-477-082-1 (1-670)
US-09-477-082-16 Sequence 16, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20. US-09-477-082-1 (1-670)
US-09-477-082-22 Sequence 22, Application US/09477082
200 X 250 X 250 X TCCGGCGGGAGGGAGGAGAGGGTGTGACTTCAGTGACTTCAGTGAGGTTTGATCAAGGGAAAGGGAAAGGGAAACTTC
                                                                                                                                                                                                                                                                                                                                                                           X 660 670
GGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 350 360 370 380 X 390 400 X CTAAAIGGAGTCAGGGCITTAGITTGCACGTCCATG
                                                                                                                                                                                                                      × Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 50 100 X
ACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGGTGGGAACTCAGCCTGAGCACGGGTTGATCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 420 430 440 ATTGTCTGCAATGCTTCTGAATGGTTGGAATTGGGCATCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 120 130 140 150 AGCAGGGCTAAGCCAAGTACGAATGAACCAGACCACTTCCTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 640 650 660 670 CTTTTGTGTTTTTTTTCGAGCCATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50%
8
                                                                                                                                                                                                                                                                                                                                                                                                                                      8 Optimized Score = 11
47% Matches = 11
0 Conservative Substitutions
                                                                7 Optimized Score = 9
45% Matches = 9
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 Optimized Score = 12
54% Matches = 12
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 Significance = -0.22
12 Mismatches = 10
1tions = 0
                                                                  9 Significance = -0.23
9 Mismatches = 11
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                            11 Significance = -0.22
11 Mismatches = 12
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 Significance = -0.22
11 Mismatches = 11
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCGGGTTTTCCCGAGGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCACAGGTAGCACGGAAAACC X 10 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTACAGGTGGGAAACTC
X 10 20 X
```

CCCAACCACAAAGGGTCATG

```
Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                                                               10. US-09-477-082-1 (1-670)
    US-09-477-082-5 Sequence 5, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                  AČTGTCCAAGGGGAGTGGTTTCCGTTCAACTCTAAATGTCTAG
730 X 740 750 760 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCTCCCATGGAGACAAGGGCATCATCTATGGCACTGATGGAGAGCCCCCCCATCTATGAGCTGACAT 240 250 260 270 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTATĠACATTTTĠAÀ-----ÀÁTĊTÀCCAÀĊTCATĠGÀCCACÁGTAÁCATGGAĊTGCTTCATĊTĠCTGTÀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTÁCTATCTACTCÁTATTCAGAGCCTATTÁGAAAGTGCTATGTGATTTAGATCÁCATTAACAGGTCÁGÁGA
660 700 710 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTTCCTAÓCGAAÁCCĆTGCÁGÁGGGAAĆCTĠGTACÁTCCÁGTĆACTTTGCCAGAĆĆCTGAGAGAGAGGGATG
520 530 540 550 550 560 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCTTCTCCTTTATCCTCTCACTTCTGTCTTTCTGGGCCAGAAAACATGGAATCGCTTCCCTAGTAGCCTG
                                                  280 390 340 CCCAGAÇÇÇTTTGCAAGAAGAATGGCATAFTAÇTTAÇTÇÇÇÇCCGAÇAGGGGTTATTAÇTAAATGGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 460 470 480 490 500 510 520 ATTOCTOTITAAACAGGAAACATTTCTTGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 320 330 340 350 360 370 ATTACTAAATGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     севеттватсевая всавеста авсера в пасва автора в сереттестесттттте па в сереттвательного в постать по в пасва в
                                                                                                                                                                       380 390 440 410 420
AGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGC
AGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCACATCCCTCTTCTGAATGGTTGGAATTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCGGTAAGTTTTGCCTACTCAGCCCTCCTCACTGTTACAC----TACCTTCCCCCCCCTACTCCATCAC
                                                                                                                                                                                                                                       17
33%
17
                                                                                                                                                                                                                      Matches
Conservative Substitutions
                                                                                                                                                                                                                                                                             Optimized Score =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640
                                                                                                                                                                                                                                         GGGGÁCTGÁGTGÁCATCTGÁCA
X 10 20
```

Residue Identity = Gaps =

718

10 Optimized Score =

15 Significance = -0.21 15 Mismatches = 6

00

Conservative Substitutions

13. US-09-477-082-1 (1-670) US-09-477-082-18 Sequence 18, Application US/09477082

```
Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                                                                                                               12. US-09-477-082-1 (1-670)
US-09-477-082-20 Sequence 20, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score = Residue Identity = Gaps = Figure 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11. US-09-477-082-1 (1-670)
US-09-477-082-28 Sequence 28, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        350 360 370 380 390 400 400 GTATAAAGCATGTCÇAÇGCCTCGGGCTTTAGTTTGÇAÇGTÇÇATGAAÇTÇTCTGCCAC
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GGAGCCAGATTCTGCCTTTACGCTGGAGGG-------AAGTGTTTTCACAGGTTCTCCTCCT
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                                                                                                                                .80 190 200 210 220 230 240 250
CACAGGGCTGACTTTACCCAGTCCGGCGGGAGGAGGAGGAGGGCTGGTCTGTGACTTCAGTGCTGAGGTTTG
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390 400 410 420 430 440
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.0 320 330 340 350 350 360 370
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240 250 260 270 280 290 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      630 KTTTATCTTTTGTTTTTTTCGAGCCATGGGGGTTAAAAAAAGCGCTTT
                                                                                                                                                                                              11 Optimized Score = 14
66% Matches = 14
0 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                     14 Significance = -0.20
14 Mismatches = 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 Significance = -0.19
12 Mismatches = 10
                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGAATAGTTTGCAGAGGCGAT
X
                                                                     TTTGCCTTATCTGAGGAGAGA
X 10 20
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Initial Score = 25 Optimized Score = 220
Residue Identity = 36% Matches = 247
Gaps = · 13 Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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US-09-477-082-8 Sequence 8, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAACCTCGGGGGATACTGTCTGATCATCCAACAATCACAATTTTGCAAAAGCACGGGAGAAAGTGCCCAAA
280 290 300 310 320 330 340
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АСААССАСССССТСССААСТСААДТТТСВААСААССССААССАТСССАСССТСАСССТСАССССС</u>
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                                                                                                                                                                                                                                                                                                                                       GTGGGGTAÁTGACAATÓTCGGAACTCTCCAAGÁGAÁCAÁGGATÁGTGÁÁTCCCCAGGTÁGCACGGÁAAÁCCTCCA
60 70 80 90 100 110 120
GGGCATCTCTGTTCCTTTAAACAGGAAACATTTCTTGTTCGAGT--GAGTCATCTCTGTTCTGCTTTAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCAAAAGGGCCÁTGGTTCAAGAAAATÍGGATTAAACATÁTTTCCTTGTGGAGGTAAAGAACATTCTTATA
.90 500 510 520 530 540 550 560
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210 220 230 240 250 260 270
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GAGGGCTGGTCTGTGACTTCAGTGCTGAGG
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90 110 120 130 140 16GGACCACGGGTTGATCCGGAGCAGGGCTAAGCCAAGTACGAATGAACCAAGACCACTTCCT
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                                                                                                                                                                 220 Significance = -0.08
247 Mismatches = 420
tions = 0
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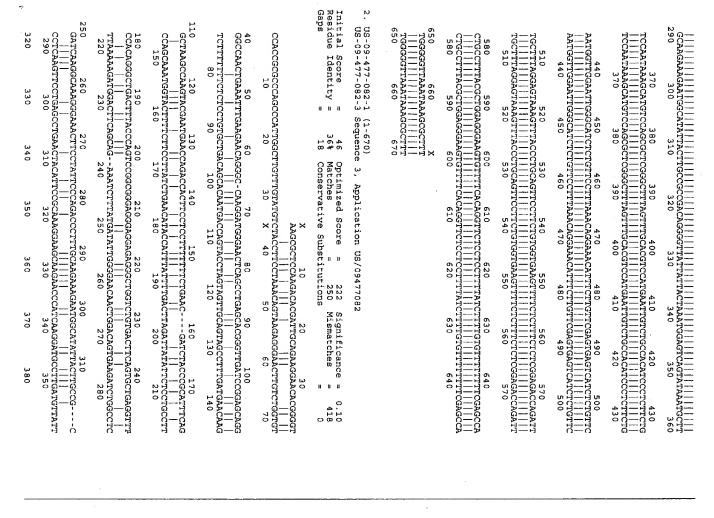
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Initial Score = Residue Identity = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial Score = 24
Residue Identity = 37%
Gaps = 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8. US-09-477-082-1 (1-670)
US-09-477-082-10 Sequence 10, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                      9. US-09-477-082-1 (1-670)
US-09-477-082-9 Seguence 9, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480 490 500 TIGITICGAGIGAAGITAAGITITACCCIGCAGITCCTTCTGTGGTGAAGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 670
TAAAĢCĢÇȚTT
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780 X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCAGGCCCCAGTTCTCCGCTGCTTTCCCCCTCAGCCGTCGCAATAGTGTGTGAATAGTTTGCAGAGGCGAT
30 40 50 60 70 80 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 280 290 300 310 X 320 330 GAAACTTCCTATTCCCAGACCCTTTGCCAAGAAAGAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTCTGTGGAATGTATTAGGCGATGAAAATGCTGGTGGGATCAAAG--CCTTATAGAGGCTGCATTTTTACA 710 720 730 740 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAAGTTTACCCTGCAGTTCCTTCTGTGGTGAAGTTTTCTCTTTTCTCTCGGAGACCAGATTCTGCCTTTACG
                                                                                                                                        TGTCCTGCACTCTCCCTGCTGGTGGTGGTGGTGTAGTGTGGCGTÅCTGTTCCACTTTTC
30 40 50 60 70 X 80 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              560 570 580 590 TTCTCTCTCGGAGACCAGATTCTGCCTTTACGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTGTCTGCCACATCCCTCTTCTGAATGGTTGGAATTGGGCATCTCTGTTCCTTTAAACAGGAAACATTTC
                    AGGGGCTTTGACCACGACTTTGAAGAGCTTCATTTTGAGATCAAGCCCCACGATGACTGCACAGTAGAGCCAA
                                                                    agaag----Gaacacgggtggccaactgaaatttgaagaacagggccaaggatgggaactcagcctgagca
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Optimized Score = Matches =
                                                                                                                                                                                                                                                                                          Conservative Substitutions
                                                                                                                                                                                                                                                                                                                    Optimized Score = Matches =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130
130
140
                                                                                                                                                                                                                                                                                                                    222 Significance = -0.10
255 Mismatches = 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 Significance = -0.09
86 Mismatches = 137
ions = 0
                                                                                                                                                                                                              x 10 20
AAGCGCTCCAAGACACGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCGTGGTCTGTCTCTGGGCC
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Initial Score = Residue Identity = Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4. US-09-477-082-1 (1-670)
US-09-477-082-4 Sequence 4, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACCTTTTTGTCCTCCAAGCTTCCCTGCCGCCTCGAATGCAGATACACGGACTCCCTTCTGTGGACCCGTTT 360 370 380 390 400 410 420 420
ACTGGATGÁTGÁCAÍTGGTGÉCTTGGGÁACAGCAGGCCACAATÍCTAAGCTTCTACAG--AAAAGACAGÍAGTG
330 340 350 360 370 380
                                                                                                                                                                    290 300 310 350 360
GCAAGAAAGAATGGCATATTACTTGCCGCCGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGGTTT
                                                                                                                                                                                                                             370 380 390 400 410 420 420 TCCAATAAAGCATGCAGCGTCCAGCATCCAGCATCCCTCTTCTG
                                                                                                              TTCAGAAGAAGTGAGCAGATCAGAATTGAGGTCTTTTAAGTTTTCTTTTTGCAAGAGAGAAATCTCCAAATGCAA 260 270 280 290 300 310 320
                                                                                                                                                                                                                                                                                                                                                                                               AAACAAGTTCTCTAAACGTTTTCGATGTGGATTCGCGGAAAATTAACCTGCACCCGTTTGCAAAATGAACTT 650 60 700 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650 K
CATGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 590 600 610 620 620 630 630 FTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCATGCCATTACTGGCTTTATGTTGAGGGTGGCCTTTGGGATCCGAGCCCCCTGTGGGCTCCATATATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCCGACTGGAAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGTCACTCTTTAGGCACTCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCGCTCCAAGACACGATTGCAGAAGGAACACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTITATICIG-TCATICIGAATCACGAATGCCCTGAAGGTGCACAGCCCCTTTCCCCCTCTTCGCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
36%
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CÓGCGCGTTGGCCGATTCATTAATGCAG--CTGGCACGCACGTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 Significance = -0.01
231 Mismatches = 399
```

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Initial Score = Residue Identity = Gaps = =
                                                                                                                                                                                6. US-09-477-082-1 (1-670)
US-09-477-082-7 Sequence 7, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5. US-09-477-082-1 (1-670)
US-09-477-082-6 Sequence 6, Application US/09477082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGGGTTAAATAAAGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAAACATTACTTAGAGGTATGCTGAAGTTATAATAGAGTTTTTTCTAAGT
$10 620 630 640 650

        AAGCGCTCCAAGACACGATTGCAGAAGGAACACGGGGTGGCCAACTGAAATTTGAAGAACAGGGCCAAGGAT

                                                                                                                                                                                                                                                               460 470 480 490 TGTTCCTTTAAACAGGAAACATTTCTTGTTCGAGGGAGTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGCCGCCGACAGGGGTTATTACTAAATGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTG----GCAAAATCGGCTÁCCATATCACAGGTGTTTTTAGTCAACTGTTGTTCGGGGGGTACCCTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCATTTCAGCCACAGGGCTGACTTTACCCAGTCCGGCGGAGGAGGAGGAGAGGGCTGGTCTGTGACTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 590 600 610 620 630 640
CTGCCTTTACGCTGGAGGGAAGGGTTTTCGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGAGĀGAĀACCĀCATTCĀGTATCACTTGGGAĀGCTTTGGGĀĀG-----ATGTCCCĀCCGGAGCCĀGĀTT
                                                                                                                                                                                                                                                                                                                     TGGTACCTGCATGTGTTCTCCCCTTCAGCCTTCTACCACACATGCACATCTTAACGTGCCTGCTCTACT
170 180 190 200 210 220 X
                                                                                                                                                                                                                                                                                                                                                                                                                                   31 Optimized Score = 80
37% Matches = 86
4 Conservative Substitutions
                                                                                                              3525
0*5
CÓGGICACCCTIGGÓGIAAAITITICCCGÓGGITTTTCCCGÁGGGÓGAGGÁGITGT
X 10 20 30 40 50
                                                                                                          Optimized Score = 62
Matches = 62
Conservative Substitutions
                                                                                                            62 Significance = -0.08
62 Mismatches = 115
ions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Significance = -0.03
Mismatches = 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGCCTCTACTAAGTTTTGAT
X 10 20
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Initial Score = 36
Residue Identity = 36%
Gaps = 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3. US-09-477-082-1 (1-670)
US-09-477-082-2 Sequence 2, Application US/09477082
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720 730 740 750 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530 540 550 560 570 580 590 CTGCAGTTCTCTGTGTGAGGGAAG
390 410 420 430
TTTCCAATAAAGCATGTCCAGGGCTCGGGCTTTAGTTTGCACGTCCATGAATTGTCTGCCACATCCCTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARTTCTÁAAGCTTCTACAGAAGACÁGTAGTGCCTTGGTGGTCCTGCTAAAGGCTGTAAAACTTAGCTTCTC 650 660 670 670 880 690 700 710 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACAGCCTCTGAGCTGATTGGGGCTTTTTTTTGTGGTACCCTGGCTAGTGCCTGGGAACCCAGCAGTGCCA
580 590 600 610 620 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 300 310 320 TIGCAAGAAAATGGACAAGGGGTATTAATTACTAAATGGAGTCAGTATAAATGC
                                                                                                                                                                                                                                                                                     GTGGGGGTGGGGAAGCAACTTGGATCTGCCCTTCTGAGGACACCTCTGGTGCTGGCCCTGGCCCAGGTCTCCTG
                                                                                                                                                                                                                                                                                                                                                                  220 230 240 250 250 260 270 280 260 270 280 260 270 280 280 270 280 280 270 280 280 270 280 280 280 280 280 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150
TCCTTTTTTTCTGAACGAȚCTĂCCCGCĂTTTCĂ-GCCĂCAGGGCTGACȚTTĂCCCAGTCGGCGGGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGTGGAGTTAGGCAG-GTTAGGGGAACTCGGAAGACTGCGATGGTGCCAAGGAAAGGGTGGAGCGGGTGAGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGAACTCAGCCTGAGCAGGGTTGATCCGGAGCAGGCTAAGGCAAGTACGAATGAACCAGACCACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCAGGGCTCAAATTTCTGCCTACAGGTGGGTGGAAACTCCCATTGTGGGAACTGGGAAGTGTGGGTTGAAT 510 520 530 540 550 560 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 480 500 510 520 TTAAACAGAAAACATTTCT-----TGTTCGAGTGAGTCATCTCTGTTCTGCTTTAGGAGTAAAGTTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGACAGGGGTTATTATTACTAAATGGAGTCAGTATAAATGCTTTCCAATAAAGCATGTCCAGCGCTCGGGCT
                                                                                                    TGTGGTTTCTCTCTGAGCCGATGCCTTTGACTTTTGCTACTTTTTCACTCTGAGCAGTCTCCAGTTCCTCTGC
290 300 310 320 330 340 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARTTAGA CGCGTATTGALAGTAAAAGTACTTCTTCCTGLGGAGGCCTTTCCCACCCCCTTCCCTGLGACAX
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70 г. досторова в применения в п
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Optimized Score = 219
Matches = 243
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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243 Mismatches = 424
tions = 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            v <u>0 v</u>
0 <u>0</u> v
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                                                                                                                                                                                                                                                                                                                                                                                  SEOUZEGOES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query sequence being compared:US-09-477-082-1 (1-670)
Number of sequences searched: 32
Number of scores above cutoff: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastDB -
Release 5
  Sequence Name
                                A 100% identical sequence to the query sequence was found:
                                                       The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                  Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            чО
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                                                                                                                                                          Times:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Results of the initial comparison of US-09-477-082-1 (1-670) with: File : US09477082.seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Fast Pairwise Comparison of Sequences 5.4
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Joining penalty
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1. US-09-477-082-1 (1-670) US-09-477-082-1 Sequence 1, Application US/09477082

290 300 350 360 390 390 390 390 390 390 390 390 390 39	220 230 230 240 250 250 260 270 280 250 260 270 280 270 280 280 270 280 280 270 280 280 270 280 280 280 280 280 280 280 280 280 28	150 CCTTTTTTCTGAACGATCTACCGCATTTCAGCCACAGGCTGACTTACCCAGTCCGGCGGAGGAGGA	80 90 140 GGGAACTCAGCCTGAGCACGGGTTGATCCGGAGCAGGGCTAAGCCAGGTACGAGTACGAACCAGACCACTTCCT	X 10 AGCGCTCCAAGAACACGATTGCAAAAGGAACACGGGGTGGCCAACTGAAATTTGAAAGAACAGGGCCAAGGAT	Initial Score = 670 Optimized Score = 670 Significance = 5.46 Residue Identity = 100% Matches = 670 Mismatches = 0 Gaps = 0 Conservative Substitutions = 0	
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